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82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGGCCTACC 141
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; Sequence 822, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICAMT: Xu, Jiangchun
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
    TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
    FILE REPREMENT 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; MUMBER OF SEQ ID NOS: 982
; SEQ ID NO 822
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-822-827-822
                                                                                 THE THERAPY AND
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APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER,
FILLE REPERRENCE: 210.121.427.224
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SET IN NO 822
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Mismatches:
Indels:
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653.00
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; ORGANISM: Homo sapiens
US-09-780-669-822
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Best Local Similarity:
Query Match:
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US-09-822-827-822
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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        CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (FILE REFREENCE: 210121,427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 922
LENGTH: 675
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Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Nu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hangy Yuqui
APPLICANT: Hangy Yuqui
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Skeiky, Yasir A.W.
Hepler, William
Hural, John
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Vedvick, Thomas
Carter, Darrick
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-780-669-822
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; Sequence 822, Application US/09895814; Publication No. US20020193296A1; GENERAL INFORMATION:
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Rolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aljun
Skelky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-822
                                                                                                          Percent Similarity: 6
Best Local Similarity: 10
Query Match: 10
DB:
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US-09-895-814-822
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APPLICANT: Mitcham, Jennifer L.

APPLICANT: Matcham, Jennifer L.

APPLICANT: Matcham, Jennifer L.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Skeiky, Zadir A.W.

APPLICANT: Wang, Ajun

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Fonger, Gary R.

APPLICANT: Panger, Gary R.

APPLICANT: Panger, Gary R.

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF SEQ ID NOS: 982

CURRENT APPLICATION: WINDER: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 822

LENGTH: 675
  675
128
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                       US-09-684-215B-18 (1-128) x US-09-822-827-822 (1-675)
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Publication No. US20020192763A1
Publication No. US20020192763A1
Publication No. US20020192763A1
Publication No. US20020192763A1
Publication No. Holds No. Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Horderson, Robert A.
APPLICANT: Horderson, Robert A.
APPLICANT: Moneill, Patricia D.
APPLICANT: Horderson, Raymond L.
APPLICANT: Fovy, Tersea
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
  675
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: MONAill, Patricia D.
APPLICANT: HOUGHION, RAYMOND L.
APPLICANT: Vinals de Bassols, Carlota
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Alignment Scores
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Matches:
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 922
LENGTH: 675
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PUBlication No. US20020183251A1
PUBLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Garder, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Ailun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Mang, Ailun
APPLICANT: Mang, Ailun
APPLICANT: Mang, Ailun
APPLICANT: Menderson, Robert A.
APPLICANT: Mondition, Raymond L.
APPLICANT: Milliam T.
APPLICANT: McNeill, Patricia D.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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CORGANISM: Homo sapiens
US-09-895-814-822
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                               THE THERAPY AND
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APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 10121.427027
CURRENT APPLICATION NUMBER: US,10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FRALSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 822, Application US/10144678A
PUBLICANTON NO. US20030157089A1
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ranger, Yuqiu
APPLICANT: Ranger, Yuqiu
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 ACATTGGCCGAGGGACCCCCGGCC 405
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CRGANISM: Homo sapiens
US-10-012-896-822
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Best Local Similarity:
Query Match:
DB:
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GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
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US-10-294-025-822
Squence 822, Application US/10294025
Squence 822, Application US/10294025
Squence 822, Application No. US20030185830A1
GENERAL INFORMATION:
Jangchun
APPLICANT: Xu. Jangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427029
CURRENT APPLICATION NUMBER: US/10/294,025
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APPLICANT: Skeiky, Yasir A. W. APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Hural, 'Ohn T. APPLICANT: Hural, 'Ohn T. APPLICANT: Hural, 'Ohn J. APPLICANT: Houghton, Raymond L. APPLICANT: Vinals y de Bassols, Carlota APPLICANT: Vinals y de Bassols, Carlota APPLICANT: Roy, Taresa M. APPLICANT: Matanabe, Yoshihiro APPLICANT: Matanabe, Yoshihiro APPLICANT: Deng, Ta APPLICANT: Deng, Ta APPLICANT: Deng, Ta APPLICANT: COMPOSITIONS OF PROSTATE CANCER TILE REFERENCE: 210121.427C28

CURRENT APPLICATION NUMBER: US/10/144,678A

CURRENT FILING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 822
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COGANISM: Homo sapiens
US-10-144-678A-822
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Percent Similarity:
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Query Match:
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1862
LENGTH: 822
TYPE: DNA
ORGANISM: Homo sapiens
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Mismatches:
Indels:
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Matches:
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Patent No. US20020168637A1
GENERAL INFORMATION:
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Enger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ren, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
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Best Local Similarity:
Query Match:
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US-09-736-457-1862
Alignment Scores:
Pred. No.:
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CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
TYPE: DNA
CORGANISM: Homo sapiens
US-10-294-025-822

us-09-684-215b-18.rnpb

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Sequence 1862, Application US/09849626

Publication No. US20020197669A1

Sequence 1862, Application US/09849626

Publication No. US20020197669A1

Sequence 1862, Application No. US20020197669A1

APPLICANT: Bangur, Chaitanya

APPLICANT: Fanger, Gary

APPLICANT: Wang, Aljun

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong
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Conservative:
Mismatches:
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               Mismatches:
Indels:
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CRGANISM: Homo sapiens
US-09-849-626-1862
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JESCUREAL INFORMATION:
Sequence 1862 Application US/09902941
JESCUREAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
JAPPLICANT: Wardanbe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Carter, Chaitanya S.
APPLICANT: Fanger, Chaitanya S.
APPLICANT: Panger, Chaitanya S.
APPLICANT: Monabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INAGMOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C17
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARRE: FastESE for Windows Version 4.0
SEQ ID NO 1862
LENGTH: 822
TYPE: DNA
CORANISM: Homo sapiens
US-09-902-941-1862
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Conservative:
Mismatches:
Indels:
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                          81 AepGlyalaProlleAenSerAlaThrAlaMetAlaAepAlaLeuAsnGlyHisFioPro
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AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
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US-10-1794-1862.

Sequence 1862. Application US/1001754

Publication No. US20030054363A1

GENERAL INPORMATION:

APPLICANT: Henderson, Robert A.

APPLICANT: Harderson, Jeffrey C.

APPLICANT: GATENDE, Yoshiniro

APPLICANT: Johnson, Jeffrey C.

APPLICANT: Retter, Marc W.

APPLICANT: Garter, Darrick

APPLICANT: Garter, Darrick

APPLICANT: Garter, Darrick

APPLICANT: Garter, Darrick

APPLICANT: Bangur, Chattanya S.

APPLICANT: Bangur, Chattanya S.

APPLICANT: MONADD, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTIONS AND METHODS FOR THE

TITLE OF INVENTIONS AND THE FOR 
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Query Match:
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; ORGANISM: Homo
US-10-017-754-1862
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US-10-017-754-1862
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                               82 GGGCAGGCGATGGCGATTCGCGGCCAGCTTCCCACCGTTCATATCGGGCCTACC 141
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          GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
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US-10-283-017-1862
Sequence 1862, Application US/10283017
Septicant: Hatanabe, Yoshihiro
APPLICANT: Ratanabe, Yoshihiro
APPLICANT: Sleath, Marcal D.
APPLICANT: Glath, Marcal D.
APPLICANT: Baths, Margarita
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Vedyick, Thomas S.
APPLICANT: Wodvick, Thomas S.
APPLICANT: Wodvick, Thomas S.
APPLICANT: Wordick, Chaitanya S.
APPLICANT: Wordick, Thomas S.
APPLICANT: Wordick, Thomas S.
APPLICANT: Wordick, Thomas S.
APPLICANT: Wordick Candria
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: UNBER: US/10/283,017
CURRENT FILING DATE: 2002-10-28
NUMBER OF SEQ ID NOS: 2157
SEQ ID NO 1862
LIENGTH: 822
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CRGANISM: Homo sapiens

US-10-283-017-1862
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; Publication No. US20030017167A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Vigitu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                  RESULT 15
US-09-878-722-236
Sequence 236, Application US/09878722
Publication No. US20020040127A1
GENERAL INFORMATION:
APPLICANT: Hepter, William T.
APPLICANT: Glapper, Jonathan
APPLICANT: Wang, Aijun
APPLICANT: Secrist, Heather
ITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
ITLING OF INVENTION: AND DIAGNOSIS OF COLON CANCER
INVERSIT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 245
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 228
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  ThrLeuAlaGluGlyProProAla
                      382 ACATTGGCCGAGGGACCCCCGGCC
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CRGANISM: Homo
US-09-878-722-236
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US-09-904-456-236
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                                                                                    GACGCCCCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCC 321
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GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
FILE REFERENCE: 210121.478C19
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FRELEGE for Windows Version 4.0
SEQ ID NO 1862
LENGTH: 822
TYPE: DNA
CREANISM: Homo sapiens
US-10-113-872-1862
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Publication No. US20030170255A1
GENERAL INFORMATION:
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US-10-113-872-1862
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APPLICANT: Rain, Ligun
APPLICANT: Raine, Ligun
APPLICANT: Raines, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hower, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Washer, Nair A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: APPLICANT: Nair A.W.
APPLICANT: CAMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING BATE: 2000.12-12
NUMBER OF SEC ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
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FILE REFERENCE: 210121.524C1
CURRENT APPLICATION NUMBER: US/09/904,456
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 247
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 894
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Patent No. US20020052329A1
GENERAL INFORMATION:
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                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-904-456-236
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Best Local Similarity:
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US-09-735-705-353
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Pred. No.:
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; SEQ ID NO 353
; LENGTH: 900
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-09-735-705-353
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ORGANISM: Homo sapiens
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US-09-850-716A-353
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82 GGGCAGGCGAIGGCGAICGCGGGCCAGAICAAGCTICCCACCGIICAIAICGGGCCIACC 141
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                                                                                                                                                  61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                   AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
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US-100-007-700-353
is Septication US/10007700
spidence 353, Application US/10007701
spidence 353, Application US/10007701
spidence 353, Application US/10007701
spidence 353, Application US/100071
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CRGANISM: Homo sapiens
US-10-007-700-353
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; Sequence 353, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
    APPLICANT: Wang, Tongtong
; APPLICANT: Mannerakis, Margarita
    APPLICANT: Panger, Gary R.
    APPLICANT: Carter, Darrick
    APPLICANT: Carter, Darrick
    APPLICANT: Watanabe, Yoshihiro
    APPLICANT: Watanabe, Yoshihiro
    APPLICANT: Peckham, David W.
    APPLICANT: Penger, Noil
    ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
    ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
    ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
    CURRENT APPLICATION NUMBER: US/09/897,778
    CURRENT APPLICATION NUMBER: US/09/897,778
    CURRENT APPLICATION NUMBER: US/09/897,778
    SOFTWARE: FagetSEQ for Windows Version 4.0
    SEQ ID NO 353
    LENGTH: 900
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US-10-313-986-353
Sequence 353, Application US/10313986
Publication No. US20030236209A1
GENERAL INFORMATION:
APPLICANT: McMabb, Andria
APPLICANT: Watchabe, Yoshihiro
APPLICANT: Wang, Tongtong
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 353
LENGTH: 900
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; ORGANISM: Homo
US-10-313-986-353
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                                               AlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
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; Sequence 353, Application US/10117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
    APPLICANT: Foy, Teresa M.
    APPLICANT: Panger, Gary R.
    APPLICANT: Application US/101178.

APPLICANT: Applicant: Applicant: Applicant: Watanabe, Yoshihiro
    APPLICANT: Mericale, Barbara
    APPLICANT: Mericale, Barbara
    APPLICANT: Mericale, Barbara
    APPLICANT: Fan, Lique
    APPLICANT: Wang, Tongtong
    TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
    FILE REFERENCE: 21012.455C18
    CURRENT APPLICATION NUMBER: US/10/117,982
    CURRENT FILING DATE: 2002-04-05
    NUMBER OF SEQ ID NOS: 484
    SOFTWARE: FastSEQ for Windows Version 4.0
    TUNDOR: NN.
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ORGANISM: Homo sapiens
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US-10-117-982-353
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US-09-780-669-834

US-09-780-669-834

Sequence 834, Application US/09780669

Septicant Millon, Davin C.

APPLICANT Mitchem, Jennifer L.

APPLICANT Henderson, Robert A.

APPLICANT Henderson, Robert A.

APPLICANT Fanger, Gary R.

APPLICANT Stolk, John A.

APPLICANT Wedvick, Thomas S.

APPLICANT Wedvick, Thomas S.

APPLICANT Wedvick, Millam

APPLICANT Wedvick, Millam

APPLICANT Wedvick, Millam

APPLICANT Wedvick, Millam

APPLICANT Heyder, Willam

APPLICANT Heyder, Willam

APPLICANT Houghton, Raymond L.

TITLE OF INVENTION DIAGNOSIS OF PROSTATE CANCER

FILE REFRENCE 2101-427C24

CURRENT PLING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 943

CURRENT PLING DATE: 2001-02-09

NUMBER PRESECTED SEQ ID NOS: 943

CURRENT PLING DATE: PRESECTED SEQ ID NOS: 9784

SEQ ID NO 834

CENGRANSM: Homo sapiens

US-09-780-669-834
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Cariet, Dann A.
APPLICANT: Carter, Dann A.
APPLICANT: Carter, Dannes S.
APPLICANT: Carter, Dannes S.
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Wang, Ajun
APPLICANT: Carter, Dannes S.
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APPLICANT: Carter, Dannes S.
APPLICANT: Wang, Ajun
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Sequence 834, Application US/09759143
Patent No. U52002022248A1
GENERAL INFORMATION:
APPLICANT: Willon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hendersen, Robert A.
APPLICANT: Hendersen, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Ralos, Michael D.
APPLICANT: Reter, Marc W.
APPLICANT: Reter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Us, Samuel
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; ORGANISM: Homo sapiens
US-09-759-143-834
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                                                                         RESULT 25
US-09-822-827-834
; Sequence 834, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANF: Xv. Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT APLICATION NUMBER: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 834
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US-09-895-793-834
Sequence 834, Application US/09895793
Sequence 834, Application US/09895793
GENERAL INFORMATION:
APPLICANT: Xu, Viangchun; APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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; ORGANISM: Homo sapiens
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Best Local Similarity: 1
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APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Poughton, ComPositions AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
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US-05-985-814-834
Sequence 834, Application US/09895814
; Publication No. US20020193296A1
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CRGANISM: Homo
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81 40 201

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142 GCCTTCCTCGGCTTGGGGTGTTGTCGACAACGGCAACGGCGCACGAGTCCAACGCGTG 201
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JEDICANT:
JOILON, Davin C.
APPLICANT:
MICCHAM, Dannifer L.
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Stolk, John A.
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Carter, Darrick
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81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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REBUILT 28
Sequence 834, Application US/10012896
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Sequence 834, Application US/10012896
Sequence 834, Application No. US2020183251A1
Septicant No. US2020183251A1
APPLICANT NICHAM, Dennifer L.
APPLICANT Harlocker, Susan L.
APPLICANT Ratics, Michael D.
APPLICANT Stolk, John A.
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APPLICANT Stolk, John A.
APPLICANT Skeiky, Ajan T.
APPLICANT Workey, Milliam T.
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APPLICANT Harlocker, Walliam T.
APPLICANT Harlocker, Walliam T.
APPLICANT Houghton, Raymond L.
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APPLICANT Wateranabe, Yoshihiro
APPLICANT Wateranabe, Yoshihiro
APPLICANT Finger Gary R.
APPLICANT Fanger Gary R.
APPLICANT Fanger Gary R.
APPLICANT Mandaher, Madeleine Joy
TITLE OF INVENTION COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION COMPOSITIONS AND METHODS FOR THE PLE REPERENCE.
TITLE OF INVENTION NUMBER: US/10/012,896
CURRENT PELLING DATE: 210121.427027
CURRENT PELLING DATE: PASEEQ FOR WINDOWS 1011.
SEQ ID NO 834
LENGTH: PASE
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CRGANISM: Homo sapiens
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101 GlyAspVall1eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAshVal 120

322 GGTGACGTCATCTCGGTGACCTGGCAAGTCGGGCGGGCACGCGTACAGGGAACGTG 381

ACATTGGCCGAGGGACCCCCGGCC 405

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82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACGTTCATATCGGGCCTACC 141
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202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGACCACCGGCGACGTGATCACCGCGGTC
                            Sequence 834, Application US/10294025
; Publication No. US20030185830A1
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
; TITLE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT APPLICATION NUMBER: 20/2-11-12
; NUMBER: OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 834
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CORGANISM: Homo sapiens
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     GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
               322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCGCACGCGTACAGGGAACGTG 381
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Search completed: April 30, 2004, 05:10:24 Job time : 471.379 secs

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Title: Perfect

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April 29, 2004, 22:25:27; Search time 2507.02 Seconds (without alignments) 1524.660 Million cell updates/sec
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1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                       OM protein - nucleic search, using frame plus p2n model
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LLMGtag541 MG1363 Random Sequence Tag Library Lactococcus lactis
Subsp. cremoris genomic, genomic survey sequence.
BH770798
Silbaq.F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
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                                                                                                                                                                        Contact: Silbag FS
Microbiology
Colorado State University
Colorado State University
Fort Collins, CO 80523, USA
Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Uso
of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization of an ordered cosmid library to deduce the genomic organization organizat
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
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Bolotin, A., Ehrlich, S.D. and Sorokin, A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci., Aliments (2002) In press
Contact: Sorokin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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A linear GSS 17-DEC-2002 aeruginosa genomic clone
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas
1 (bases 1 to 959)
        en Josas cedex, France
                                                                                                                                                                                                                                                 /.organism="Lactococcus lactis subsp. cremoris"
/mol type="genomic DNA"
/strain="MG1363"
/strain="MG1363"
/db_xref="taxon:1359"
/db_xref="taxon:1359"
/clone lib="MG1363 Random Sequence Tag Library"
/clone lib="WG1363 Random Sequence Tag Library"
/note="Vector: pSGWU2; Site 1: Smal; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
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383 ATGGTTGACCTATCTCAATTATCAACAAATGATAGTTCTCAACTGAAATTACCTAGCAGC
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CRJ INRA, Domaine de Vilvert, 78352 Jouy en José Tel: 33 134 65 25 16
Fax: 33 134 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is htrA (95%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 1408.
Location/Qualifiers
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31
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Conservative:
Mismatches:
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29.85%
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1 (bases 1 to 726)

3 dantasuriyarat.

Rudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                       Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
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/note="Vector: pBluescript II KS
XhoI; Uninfected Control"
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Matches:
Conservative:
Mismatches:
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BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: P column: 19
Seq primer: gga aac agc tat gac cat
Location/Qualifiers
                                                                                                                                                                                                                                                                                  Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'tissue_type="Leaf"
'dev_stage="3 week"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0126
122.50
42.86%
30.83%
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Fax: 520 621 9288
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OSJNEf02F19.r OSJNEf Oryza sativa (japonica cultivar-group) cDNA
Clone OSJNEf02F19 3', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:287"
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                                ğ
                                multiple isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pseudomonas aeruginosa"
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/strain="1-60"
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Matches:
Conservative:
Mismatches:
Indels:
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
                              Whole-Genome-Sequence variation among
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
             Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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Length:
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(1-590)US-09-684-215B-18 (1-128) x CB925602 GlyPheAlaileProileGlyGlnAlaMetAlaileAlaGlyGlnIleLysLeuProThr 34

SCGGFL3058G06.g Saccharum officinarum FL3 Saccharum officinarum CDNA clone SCGGFL3058G06 5', mRNA sequence. 170 54 ATTCAGTTCGGAAAAGTTCGTCGTGCTGGCTTGAAT---GTGGACTTCGCTCCGGATCCA 110 291 GTTCTGGATGACTATGGCGTCGGAGATCAGGTGACCTTGACA------ 332 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD Clade, Panicoldeae, Andropogoneae, Saccharum. 94 AlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGly 113 74 GIYASPValileThrAlaValAspGIYAlaProlleAsnSerAlaThrAlaMetAlaAsp 93 64 73 111 ATTGCATATCAGCTTAAAGTTCGCAACGCAGCTCTTATACTTAAGGTACCTGGGGGAGT ||||||||:::||| 231 GGTGATATCATCGTTGCAGTGGAAACCTGTTAAGGGCAAATCTGACCTGAGG 50 ------AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAla 65 ProAlaAlaSerLeuGlyIleSer-----Thr FEATURES

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cultivar="Kennebec or Binjte"

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	ores: 0.0499 Length: 807 117.50 Matches: 39 larity: 42.54\$ Conservative: 18 imllarity: 29.10\$ Mismatches: 34 17.99\$ Indels: 5	-215B-18 (1-128) x CA228900 (1-807)	0 SerginglyglyglyglaglyPhealaileProileglyglnalaMetalaileAlaglygln 29	H	::: 9 TTAATTCAGTTTGGAAAAGTTCGTCGTGCTGGCTTGAATGTGGAC 465	0	valvalGlySerAlaProAlaAlaSerLeuGlyIleSer72		ThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAla 88	A GGIAACATIGITCTTGGIGATGTCATCGTTGCAGIGGATGGCAAACCTGTTAAGGGCAAA 285		9 GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 122	ATCCGGCGAGGCTCTGAAACCC	BQ514888 To a set of potato cDNA clones for mak-2003 EST62303 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIO81 3' end, mRNA sequence. BQ514888 GENERAL GI:21373757 EST.	Solamum tuberosum (pocace) Solamum tuberosum (pocace) Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Asterids: lamiids: Solamales: Solamanese: Solamim.	., Tanksley,S.	Generation of a set of potato cDNA clones for microarray analyses Umpublished (2002) Other_ESTE: ESTES.302 Contact: Robin Buell	The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: Doctato-arrav@tigr.org	This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/	sed primer: 1/. Location/Qualifiers 1. 758	
	Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity Query Match: DB:	US-09-684-215B	Oy 10 Db 569	Qy 30	Db 509	Qy 50	09	Db 404	73	JD 344	Oy 89 Db 284	Qy 109	Db 227	RESULT 7 BQ514888/c LOCUS BQ DEFINITION BS ACCESSION BQ VERSION KEYWORDS SCHEPCE	NISM	REFERENCE 1 AUTHORS BU Re	TITLE GE JOURNAL UN COMMENT OT	17 97 83	Th In	SE FEATURES SOURCE	

/organism="Solanum tuberosum" /mol_type="mRNA"

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AZ934428 603 bp DNA linear GSS 24-APR-2001 BJ Ba0002108r B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
AZ934428 1 GI:13776488
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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Genome Res. 11 (8), 1434-1440 (2001)
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AJ558965 and GI31661537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antirrhinum majus (snapdragon)
Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AspGlyAlaProlleAsnSeralaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AAGGGTTCGGTCAGCCGCGGCTCGATCGGCGTGCAATTCAGCCGGTGACG----- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 TOGGATATOGCCGÀCAGCCTCCCCATGAAGAAGGCCGAACGCGAAGCGCGAGCCG 415
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245 GGCATCGCGTTCTCGATCCCGGCCAACACGCTGAAGACGGTTGTTGCCCAGCTCAAGGAC 304
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                                                                          1..603...
| Coganism= Bradyrhizobium japonicum" | Amoi Lype= genomic DNA" | Strain= USDA110" | Ab xref="taxon:375" | Ab host="E. coli" | Ab host="E. coli" | Anoi Lib="B. japonicum BAC library" | Anoie="Vector: pindigo536; Site_1: HindIII"
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Conservative:
Mismatches:
Indels:
Gaps:
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    Fax: 864 656 4293
Email: rw.ing@clemson.edu
Class: BAC ende
High quality sequence stop: 553.
Location/Qualifiers
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Molekulare Pflanzengenetik
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16.23%
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pacs2-164 3239,y3 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_3239, genomic survey sequence. BZ561390 BZ561390.1 GI:27181349 GSS.
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311 ACCICGGCGGTGTAGGATTTGCGATCCTTCATCGACAGTGGTAAAGATAGTGCCTCAG 370
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Pseudomonas aeruginosa

Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.

1 (baase 1 to 1033)

Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.

Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press

Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                    50 -----AsnAsnGlyAlaArgValGlnArg
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1...765./
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/db_xref="taxon:4151"
/clone="0.18" 1.09 a08"
/tissue type="whole plant"
/clone_[lb="Antirrhinum majus whole plant"
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Mismatches:
Indels:
Gaps:
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University of Washington
Dex 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun
                                                                                                                                                                                                                                                                                                       US-09-684-215B-18 (1-128) x AJ558965 (1-765)
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104.00
42.24%
29.31%
15.93%
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Best Local Similarity:
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RESULT 12
AQ989479
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Pseudomonas aeruginosa

Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

E 1 (bases 1 to 947)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Oleen, M.V.

Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library

J. Bacteriol. (2002) In press

Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 17-DEC-2002
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                                                                                                                                                                                                                                                                                            68 erLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pacsi-60 1644.81 pacsl-60 Pseudomonas aeruginosa genomic clone pacsl-60_1644, genomic survey sequence.
BZS49047.
BZS49047.1 GI:27152628
GSS.
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                                                                                           genomic shotgun
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1. .1033

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="0-164"

/db_xref="taxon:287"

/clone="pacs2-164" 229"

/clone="pacs2-164" 229"

/note="clinical isolate 2-164 Whole gen

library."
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Matches:
Conservative:
Mismatches:
Indels:
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                  (1-1033)
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100.50
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30.43%
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GSS 14-AUG-2000
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ffrench-Constant, R. H., Waterfield, N., Burland, V., Perna, N. T.,
Daborn, P. J., Bowen, D. and Blattner, F. R.
A genomic sample sequence of the entomopathogenic bacterium
Photornhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Rfc00025 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00025, genomic survey
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                              Location/Qualifiers
1. 947
1. 947
1. Organism="Peeudomonas aeruginosa"
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/clone="taxon:287"
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/clone="taxon:287"
/clone="taxon:287"
/clone="taxon:287"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Email: craymond@u.washington.edu
Class: shotgun.
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AQ989479
AQ889479.1 GI:9648073
GSS.
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33.33%
15.31%
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ProAla 128
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Query Match:
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Tel: (44) 1225 826621
Fax: (44) 1225 82679
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. 726
//organism="Photorhabdus luminescens"
//mol type="genomic DNA"
//strain="W14"
//strain="W14"
//strain="W14"
//strain="W14"
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AGENCOURT 10214312 NIH_MGC_107 Homo sapiens cDNA clone
AMAGE:6585799 5', mRNA sequence.
BUSS7763.1 GI:22908059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525
                                                                                                                                                                                                                                                                /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1093)
1NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 AAAGCCGGTATTAAAGTGGGTGATATCATTACCAGCGTCAATAACAAACCGGCTATTTCT
                                                                                                                                                                                                                     dev stage="primary phase variant"
/clone lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                   726
338
17
17
23
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-726)
                                                                                                                                                                                             /db_xref="taxon:29488"
/clone="PLG00025"
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Homo sapiens
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15.16%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arrec
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://fmge.llni.gov
Plate: LLCM2798 row: f column: 07
High quality sequence stop: 299.
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750 ATGGCGGGGGGCTAAGCTATCCCACGGCGCCCCGGGGCCCCAGGGTGCAGAGCCCCCAG
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98.00
37.04%
27.16%
15.01%
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Mon May

118

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msh2_5667.x1 msh Pseudomonas aeruginosa genomic clone msh2_5667, genomic survey sequence.
BZ577987.1 GI:27213048
GSS.77987.1 GI:27213048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS.

Seudomonas aeruginosa

Beudomonas aeruginosa

Bacteria; Proteboteria; Gammaproteobacteria; Pseudomonadales;

Bacteria; Proteboteria; Gammaproteobacteria; Pseudomonadales;

I (bases I to 790)

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,

Burns, J.L., Kaul, R. and Olsen, M.V.

Whole-Genome-Sequence variation among multiple isolates of

Psedomonas aeruginosa library

J. Bacteriol. (2002) In press

Contact: Chris K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 206216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

I. 770

| Nol_Lype="Genomic DNA"
| Mal_Lype="MSH"
| Mal_Lype
152 GCAGTGGATGGCAAACCTGTTAAGGGCAAATCAGACCTGCTGAGGGTTCTGGATGACTAT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 CTTGCCGCTCCAGGGCAGCACCACGCGCACCCAAGGAGGAGGTCTCGTCGTTCTTGCC
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/clone="msh2 5667"
/clone_lib="msh"
/note="fivironmental isolate. Whole genomic shotgun
library."
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                                                                                                  212 GGCGTCGGGGATCAGGTGACCTTGACA
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96.50
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29.60%
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//dachost="DRIDG"
//dlocallb="RX1"
//dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact; Faircoludes; Audiopogonees; Saccharum.

(E. 1 (Dasses 1 to 444)

(S. Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made Sucest

The libraries that made Sucest

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Contro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone distribution: clone Collection Center (BCCC) at http://www.bccenter.fcav.unesp.br

Plate: 017 row: F column: 10

Seq primer: T7 Promoter Primer.

Location/Qualifiers
                                                                                                                                              CA148171 444 bp mRNA linear EST 24-SEP-2003 SCEZZZI017F10.g RZ1 Saccharum officinarum cDNA clone SCEZRZ1017F10 5', mRNA sequence.
CA148171 GI:35048941
                                                                                                                                                                                                                                                                                                                                      Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
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92 GGCCTTGCTCCGACCGGCAGGGTTCGCTGGTAACATTGTTCTTGGTGATGTCGTT 151
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/organism="Saccharum officinarum"
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/db_xref="taxon:4547"
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                       277 CGCGCA 272
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CA148171
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229

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280

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169

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1. :551

Coganisme-"Sorghum bicolor"

/mol type="mmkn" | Coganisme-"Sorghum bicolor" |
/do xref="taxon:4558" |
/do xref="taxon:4558" |
/do xref="taxon:4558" |
/do xref="lo-"to-"to-"to-"to-"to-"to-"to-"organ: 10- to-14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                AW285527
LG1 241 G05.gl A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                274
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116 GGTCTTGCTCCAACCGGCAGGGGTTTTGCTGGTAATATTGTTCTGGGTGATATCATCGTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 69
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                                  98
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                                                                                                                      236 GGCGTCGGAGATCAGGTGACCTTGACA------ATCCGGCGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gly11eSer-----ThrGlyAspVal11eThr
                                  79 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
155
186
188
268
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: T7
High quality sequence start: 16
High quality sequence stop: 552
POLYAPES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AW285527.1 GI:6675371
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96.00
47.62$
29.76$
14.70$
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275 TCAGAAACCCTT 286
                                                                                                                                                                    119 AsnValThrLeu 122
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Best Local Similarity:
Query Match:
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Pred. No.:
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VERSION
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AW285527
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor (sorghum)

Sorghum bicolor

Sorghum bicolor

Sorghum bicolor

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

El (bases 1 to 546)

Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.

An EST database from Sorghum: light-grown seedlings

Unpublished (2000)

Londonnier-Pratt AM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tal: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@nga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="texon.4558"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
Seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
Secoli The library was made from poly-A RNA in the cloning
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                 AW285510

1G1_241_E05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA egedence.

AW285510.1 GI:6675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AATGTTCGCAACGCACTCTTATACTTAAGGTACCTGGGGGGCAGTGCTGCAAAGCA 115
                                                                                  103 ValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 122
                 83 AlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAsp 102
                                                                                                                    ------GTCATGCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ThrGlyAspValileThr 78
                                                335 GCGGTAGTGCGCGTGGCGTCGTGGGCGAC----CGAGGTCAGCACCCAGTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
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Matches:
Conservative:
Mismatches:
Indels:
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High quality sequence start: 126
High quality sequence stop: 546
POLYA=Yes.
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                                                                                                         389 ATTCAGCGAATCGTC----
                                                                                                                                                  123 AlaGluGlyProPro 127
                                                                                                                                                                                 413 GCTGAGGGTGAACCA 427
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Pred. No.:
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AW285510
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DEFINITION
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceee, Chlamydomonas.

1 (bases 1 to 543)
C.-W., Davies, J., Harris, E., Hauser, C.,
Chamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
Contact: Charles Hauser
Contact: Charles Hauser
Contact: Charles Hauser
Contact: Bass 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8179
Email: chauser@duke.edu.
/note="Vector: pSportl; Site_1: Sall, KpnI, EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSportl vector using a NotI (5'-pGACTAGTTCTCGAGGGCGCCC (T)15-3' and a Sall 5'-TGACCAGGGTCCG-3'adapters (Giboo BRL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI721127
1031054B10.yl C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 GGTGACGTCATCACCAGTATCAACGGTCGATAGGTGACGTCAGCACGAGACATCTACGAC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GlyAspValileThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 AlaLeuAsnGlyHisHisProGlyAspVallleSerValThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 GCGGTAAATAGC-----GGGCAGCAGCTGAACATCACC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .543
/organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                      677
21
12
18
3
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Matches:
Conservative:
Mismatches:
Indels:
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BI721127.1 GI:15696822
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95.50
61.118
38.89%
14.62%
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Query Match:
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BI721127
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laborator: Panopoulou G
laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1236
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: http://www.noigen.maphioxus/
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI378928 677 bp mRNA linear EST 26-AUG-2003 BFLG1 000559 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPWGp498) Branchiostoma floridae cDNA clone MPMGp49891235 5',
                                                                                                                                                 241 GGCGTCGGAGATCAGGTGACCTTGACA------ATCCGGCGAGGC 279
                                                                                                                                                                                                                                      99 HisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 118
                                          GGTCTTGCTCCAACCGGCAGGGGTTTTGCTGGTAATATTGTTGTTGGGTGATATCATCGTT 180
                                                                                                      AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 677)
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J.,
Herwig, R., Vingron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of
vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole embryo"
/dev stage="5-6 hrs (gastrula stage)"
/lab_host="B.coli, XII blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMGp499)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTAGCCACTGGGGAAAGGGGATGTG 3' (M13FSP)
Insert length: 1200
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Branchiostoma floridae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Branchiostoma floridae (Florida lancelet)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Res. 13 (6A), 1056-1066 (2003)
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Location/Qualifiers
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/db_xref="taxon:7739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI378928.1 GI:30914099
EST.
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280 TCAGAAACCCTT 291
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22683279
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BI378928
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Pred. No.:
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HVSMEm0025L21f Hordeum vulgare green seedling EST 19-OCT-2001
HVCDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEm0025L21f, mENA sequence.
B1956121. G1:16303022
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Subaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Subaryota, Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae, Triticeae, Hordeum.
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Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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Clemson University Genomics Institute
Clemson University
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Tel: 864 656 7288
Fax: 864 656 4293
Fotal: rwing©clemson.edu
Total: hq baess = 479
Seg primer: AATTAACCCTCACTAAAGGG
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/ Lab nost="You'la!"
// Clone lib="Hordeum vulgare green seedling EST library
// Clone lib="Wordeum vulgare green seedling EST library
HVCDNA0014 (Blumeria infected) "
// Fores "Veetor: pBluescript SK(-); Site_1: ECORI; Site_2:
Xhol; Morex (mla) plants were greenhouse grown in the R
Wise lab at lows State University, Ames, IA; 7 day old
green seedlings were infected with isolate 5874 of
Blumeria grammins f: sp. hordei, and leaves were harvested
24, 48 and 72 hr post-incoulation and snap frozen
(Wise).
In the TJ Close lab at the University of California,
Riverside, total RNA was prepared from each sample pool,
equal quantities of all three RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and I million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University denomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Whing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Whing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
above. For moore details on library preparation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kileinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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Organism="Hordeum vulgare subsp. vulgare"
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lab_host="TJC121"
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                                                                                                                                                                                                            /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEm0025L21f"
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quality sequence start: 5 quality sequence stop: 620 Location/Qualifiers
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I (bases I to 982)

Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Colson,P.S., Dillon,G.P., Farisas,L.P., Gregorio,S.P., Ho.P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.B., Sak,R.G., Stukart,G.C., Soares,M.B., Garsion,T.C., Kawano,T., Rodriques,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.

Transcriptome analysis of the acoelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjodquupp.
Email: verjodquupp.
This sequence was derived from the FAPESP Schistosoma mansoni EST
This sequence was derived from the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
plate: MA3-99990-M294 row: 3 column: C. .br/schisto/
plate: MA3-99990-M294 row: 3 column: C. .coation/Qualifiers
i. .982
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/mol type="mRNA"
/db_xref="taxon:6183"
/db_xref="taxon:6183"
/sex="mixed_pool"
/sex="mixed_pool"
                                                                                                                                                                                                                                                                       CD080132 989U-M294-C03-U.B MA3-0001 Schistosoma mansoni cDNA clone MA3-9999U-M294-C03.B, mRNA sequence.
295 GTGACTGGCGTCATGGGTGAC-----GGAGGTCAGCACCCAGTGGATATTCAGCGAATC 242
                                                            107 ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeuAlaGluGlyPro 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo
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/lab_host="Mus musculus"
/clone_lib="MA3-0001"
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Schistosoma mansoni
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MEDLINE
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pacs2-164_2702.x1 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_2702, genomic survey sequence.
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      LeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGly 114
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                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

(bases 1 to 1127)
Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, B.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="genomic DNA"
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/db_xref="taxon:287"
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun library."
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Matches:
Conservative:
Mismatches:
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Box 352145, Saattle, WA 98105-2145,
TE1: 2062216954
Fax: 2066857244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: craymond@u.washington.edu
Class: shotgun.
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1. .1127
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Edea mayy

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Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD

Clade, Panitooideae, Andropogoneae, Zea.

(Dases 1 to 787)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                    365
                                                                                                                                                                                                           87 ralaThralaMetAlaAspAlaLeuAsnGlyHisHisProGly---AspValIleSerVa 106
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                                                                                                                                                                                                                                                                        245 GGCTCCGGCCACCGGGCGGTCCTCGGGTTCTTGCT---GAAGCAGCAGCCATTCTCCA
                                                                                          51 AsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu---
                                                             16 Phe Alaile Proile Gly Gln Ala Met Alaile Ala Gly Gln Ile Lysteu ProThr Val
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/dlone="zkwBWa0345G06"
/clone=lb=zw 0-7.1.5_KB"
/note="vector: pBGSk-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Tel: 301-838-5843
                                                                                                                           36 HisileGlyProThrAlaPheLeuGlyLeuGlyValValAspAsn
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Mismatches:
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/strain="B73"
                              US-09-684-215B-18 (1-128) x CG322895 (1-771)
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Email: whitelaw@tigr.org
Seg primer: TF
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Other GSSs: OGOBL39TH
Contact: Cathy Whitelaw
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Class: sheared ends.
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CG322895.1 GI:34240161
GSS.
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1 (bases 1 to 771)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraeer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
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                                                                                                                                                                              -----Gly 46
                                                                                                                                                                                                                                        47 ValValAspAsnAsnGly------AsnGlyAlaArgVal
                                                   26 IleAlaGlyGlnIleLysLeu-------ProThrVal
                                                                                                                                               472 TCAAAATCGCCTACTGACCCATATATTTTAGCAGACAATCCAGCCAATTCGGAAAGTGGA
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/note="Wector: "pBGK-: Site 1: HincII, 0.7-1.5 kb
merbylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                 41 -----AlaPheLeuGlyLeu-----
                                                                                                                                                                                                                                                                                                                                                                                              81 AspGlyAlaProlleAsnSerAla 88
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                                                                                                                    36 HisileGlyProThr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other GSSs: OGODK42TH
Contact: Cathy Whitelaw
IIGR
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Class: sheared ends.
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Zea mays
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Pred. No.:
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DB: 28 Gaps: 6	QV 510 FunderCulnolyQlyGlnGlyPhanAlalperCleGlyGlnAla 23 QV 24 MethaliahalalperCorcoxQcCACCACCACCACCACCACCACCACCACCACCACCCCCTCTTGCC 511 DD 510 GTTGCCCCTCCACCACCCCCCCCCCCCCCCCCCCCCCCC	ORIGIN Alignment Scores: 19.6 Length: 703
Query Match: 14.32% Indels: 13 DB: 5	4156 (1-787) GlnalametalailealaGlydin i:::::::	93.50 93.50 41.60% Similarity: 29.60% h: 14.32%

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o	TleGlyG ATTGACA ThrValH: STTTTGG AsnGlyA: : AATA	ValAspG - - - - -	p mRNA 1 Pancreas Libra milar to SW.PM ence. Craniata; Vert Sciurognathi; ,S., Hillier,L. A., Schmitt,A. I., Cardenas,M. I., Cardenas,M. IVIII,R., Willii	ict. Kaest is Medic Mology, vouglas puencing puencing: mage.llimage.ll
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0 08 28 98 98 CD383492	Lypheali STTTTGCJ STTTTGCJ InlleLyi :::: SGGTGGT' Jyvalva' :: SGATA CTGCTCT'	BPValil ::: ::: 	600 b Liton Mouse E16 5 RAGE:5646194 5' si TEIN. ;, mRNA sequ BI:12646670 (house mouse) ttazoa; Chordata; cheria; Rodentia; c 600) addows, A. Clifton ttin, J., Blistain, nko, I., Bennett, J nko, I., Bennett, J	d Pancreas EST Pr glass Melton, Klau norses Melton, Klau norses Consortium ersity, Howard H cular and Cellula -1812 -1857 onebiotp, harvard constructed by D niversity Genome clone please cont arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu) arvard.edu)
92.00 40.00% 26.92% 14.09% 14	SerdinGlyGlyGlyGlnGlyPheAlaileProileGlyGlnAlaMetAlaileAla ::: GCCTCGGCCGGTATTGCAATCCCAATTGACACCGTGAAATTTATTGTCGAGACG	IleSerThrGlyAspValIleThrAlaValAspGlyAlaProlleAsnSerAlaThr :::	A TO O B TO TO SEE TO S	Washu-Harvard Pancreas EST Project Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Insi Dept of Molecular and Cellular Biology, 7 Div. MA 02138 Tel: 617-495-1812 Fax: 617-495-8550p. harvard.edu Library was constructed by Dr. Douglas Melton Washington University Genome Sequencing Cente- Obsining a clone please contact: Juliana Bro (brown@fas.harvard.edu) MGI: 852914 This sequence now available from 'McDiching a clone and a contact: info@image.linl.gov Seq primer: -40RP from Gibco High quality sequence stop: 455.
	Gangly(Carce) Carregace Carregace Carregace Carregace Agecace Agecace Agecace Agecace	-Ileser' ::: 3GTAGAA aMetAla ::: TTTGTTT rLysSer cGGGTTTC	BG143271 ia95h02.y1 Mc CDNA clone IN RECEPTOR PRO' BG143271.1 GBT. BG143271.1 GBT. BMIS musculus Mus musculus Mus musculus I (bases 1.1 Mollon,D., M Wylie,T., Mas Ritter,E., R MCGARN,R., C MCGARN,R., C BOWERS,Y.	WashU Harvard Unpublished (Contact: Paul Barvard Unive Bept of Molecy MA 02138 Tel: 617-495- Fax: 617-495- Email: dmelto Library was c Washington Un Obtaining a C (brown@fas.ha MGI:185214 T MGI:185214 T MGI:185214 T High quality
e: Socal Similarity: Local Similarity / Match: 9-684-215B-18 (1-	10 Sea 178 GCC 28 238 CTC 43 61 Va 346 CCC	71 406 90 110 525		Washur Unpubli Contact Endocat Brandar MA 02 01 MA 02 01 MA 02 01 MA 03 01 Mashur Washur Washur Washur Chray Mail 18 Chray Chray Mail 18 Chray Mail 18 Mail 18 Chray Mail 18 Mail
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HS1 7 H09.bl A012 Heat-shocked seedlings Sorghum bicolor cDNA clone HS1 7 H09.bl A012 3', mRNA sequence. CD204316.1 GI:30933230 CD204316.1 GI:30933230
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidaee; Andropogoneae; Sorghum.
1 (bases 1 to 701)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
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Conservative:
Mismatches:
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Gaps:

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FEATURES

Db 288AGGGACAAGGTCGATTAAAGTTCTTGTCAAAAGAGCGAGC 335 Qy 119 AsnValThrLeu 122	Intile Mattonia Institutes of Health, Manmailan Gene Collection (Mac) Contact: Robert Strausberg, Ph.D. Email: Captbe-remail.inh.gov Tisaue Procurement: ATC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Biosciance Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llni.gov k column: 10 High quality sequence start: 12 High quality sequence story: 552. High quality sequence story: 552. Mol type="MRNA" // Mol type="MRNA" // Mol type="MRNA" // Abaref="texaon:9606" // Clone="Image: 600" // Clone="Ima	/tissue_type="teratocarcinoma, cell line" /lab.bost="NHIOB (phage-resistant)" /clone_lib="NIH_MGC_109" /note="Organ: ovary; Vector: poTB7; Site_1: EcoRI; Site_2: /note="Togan: ovary; Vector: poTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oliqo-dT priming. Directionally cloned into EcoRI/AhOI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	Alignment Scores: Pred. No.: Score: Score: 91.00 Matches: 91.00 Matches: 40 Conservative: 13 Best Local Similarity: 30.08\$ Query Match: 13.94\$ Indels: 08-09-684-215B-18 (1-128) x BU553475 (1-1098)	Qy 23 AlaMetAlaileAlaGlyGlnileLysLeuProThrValHisile 37	Qy 38 GlyproThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn 53
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Buchanan,C.D., Bastman,A. and Pratt,L.H. An EST database from Sorghum: heat-shocked seedlings JOURNAL Unpublished (2003) CONTACT: Cordoniler-Pratt MM Laboratory for Ganomics and Bioinformatics Chaiversity of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA The Thirry Constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University, sequence; plant material and RNA prepared at Texas A & M University, sequenced in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude poly%. Seq primer: Sug3 (CGACCTGCAGCACAA)	FEATURES 170 1	Alignment Scores: 24.9	Db 3 THIRD THIS CONTROL OF THE ANALYSIS AND A STANDARD A STANDARD A STANDARD AND A STANDARD A STAN	Qy 59 ArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThr 78	Qy 79 AlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 98

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                                                                                                                                                                                                                                                                                                                                           CF512107 631 bp mRNA linear EST 09-SEP-2003 6Abud0004 IVR B10 Vitis vinifera cv. Cabernet sauvignon (Clone B) Bud - CABUD Vitis vinifera cDNA clone CAbud0004_IVR_B10 3', mRNA sequence.
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Suratyora, Virialplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Virialphyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
I (bases 1 to 631)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and
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                                           68 SerLeuGlyIleSerThrGlyAspValileThrAlaValAspGlyAlaProlleAsnSer 87
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5'-ATTCTAGAGGCCGAGGGCCACATGT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
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Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-A 17 24-SEP-2003;
CORIXA CORPORATION (US)
Location/Qualifiers
1. 1872
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Search completed: April 30, 2004, 02:25:07 Job time : 3732.05 secs

Title: Perfect score:

Sequence:

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Patent No. US2002002248A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIO
                                                                                                                                      -09-759-143-822
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                                                     // Search time 469.129 Seconds
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1234.209 Million cell updates/sec
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1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              2936184 seqs, 2261732022 residues
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Listing first 45 summaries
                                                                                              April 29, 2004, 22:43:07
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic

April 29, 2004, 23:03:22; Search time 291 Seconds (without alignments) 5781.053 Million cell updates/sec Run on:

US-09-684-215B-3 Title: Perfect :

1 acggccgcgtccgataactt.......tggccgagggaccccggcc 396 score: Sequence:

IDENTITY NUC Gapop 10.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:*
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2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2011as:*
5: geneseqn2011as:*
6: geneseqn2012s:*
7: geneseqn2013as:* geneseqn2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn20048:*

SUMMARIES

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	AAL40769 AAL40772
DB	 41 41 C
Len	396
Query Match	0.001
Score	1 9 9 9 1 6 6 6 1 6 6 6
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Description	Aal40769 Nucleotid	Aal40772 Nucleotid	9	Aal40770 Nucleotid	Abk14140 DNA encod	æ	_	9	Aad28337 Mycobacte	Aax34251 Mycobacte	7	_	Ada26353 Mycobacte	Aad47084 Mycobacte	m	_	Abk14128 DNA encod	Aaz20194 Mycobacte	Aad47083 Mycobacte	Aad28342 Mycobacte	ø	32	Ada26358 Mycobacte
đΙ	AAL40769	AAL40772	AAZ20206	AAL40770	ABK14140	AAD47078	AAD47077	AAD28336	AAD28337	AAX34251	AAX34252	AAL40771	ADA26353	AAD47084	AAD28343	AAL40773	ABK14128	AAZ20194	AAD47083	AAD28342	ADA26360	ADA26359	ADA26358
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	100.00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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396	396	396	396	396	396	396	396	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	394.4	392.8	391.2	391.2	391.2
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	6	40	41	42	43	44	45

ALIGNMENTS

AAL40769 standard; DNA; 396 BP AAL40769 ID AAL4 RESULT 1

AAL40769;

(first entry) 03-OCT-2002 Nucleotide sequence encoding Ra12 protein.

Ral2, serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified

/*tag= a /product= "Ral2 protein" /note= "No start or stop Location/Qualifiers 1. .396 /*tag= a Key

codon

WO200125401-A2

12-APR-2001.

06-OCT-2000; 2000WO-US027652

99US-0158585P 07-OCT-1999;

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27.

P-PSDB; AA022138.

Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Claim 1; Fig 2; 39pp; English.

The invention relates to a recombinant nucleic acid molecule encoding efusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kDa C-terminal fragment of serine protease antigen MTB32A of

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Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another can be used in vivo as a DNA vaccine. This polynucleotide sequence and represents the DNA encoding the Ral2 protein
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06-OCT-2000; 2000WO-US027652.

WO200125401-A2.

12-APR-2001

99US-0158585P

07-OCT-1999;

Skeiky Y, Guderian J; (CORI-) CORIXA CORP.

WPI; 2001-266299/27. P-PSDB; AAO22141

Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;

Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

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                                  0; Gaps
Length 396;
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100.0%; Score 396; DB 4;
100.0%; Pred. No. 5.2e-84;
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Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds. Mucleotide sequence encoding Ral2-mammaglobin fusion protein. AAL40772 standard; DNA; 672 BP (revised)
(first entry) Mammalia. Unidentified. 06-AUG-2003 03-OCT-2002 AAL40772; AALAO772 AAL RESULT

/*tag= a /product= "Ral2-mammaglobin fusion protein"

Location/Qualifiers

Chimeric.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kbaic nolypeptide, comprising a polynucleotide sequence of Ral2, and a heterologous polynucleotide sequence.

Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies for use an antigen for monitoring binding of serum antibodies to fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses.

The coding sequences can be ligated with a coding sequence of another molecule such as a plax vaccine. This polynucleotide sequence can be used in vivo as a plax vaccine. This polynucleotide sequence can be used in vivo as a plax vaccine. This polynucleotide sequence of no 6-AUG-2003 to correct OS field.) Ö 240 120 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360 85 GGGCAGGCGATGGCGATCGCGGCCAGATCGGATCGGGTGGGGGGTCACCCTTCAT 144 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACAACGGCGCACGA 180 204 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACGCCGATGGCGGACGCGCTTAAC 300 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324 384 9 25 Acceccecerceanharenrecaerrereceachecachecanireceanneceanneceanneceanne ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAAAAAAGGGCAACGGCGCACGA 1 ACGCCCCCCCCATAACTTCCAGCTCCCAGGCTGGCCAGGATTCGCCATTCCGATC GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 25 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACCACGT Gaps ö Length 672; Sequence 672 BP; 160 A; 185 C; 187 G; 140 T; 0 U; 0 Other; Indels Query Match
100.0%; Score 396; DB 4; Sest Local Similarity 100.0%; Pred. No. 5.4e-84; Matches 396; Conservative 0; Mismatches 0; ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420 Disclosure; Fig 5; 39pp; English. 121 145 181 241 301 361 d d ò 셤 ઠ q à 임 ઠ ठ ઠે

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                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence includes a coding region for a recombinant Mycobacterium tuberculosis bi-antigens Ra12 and DPD. The DNA is useful for the motigens Ra12 and DPD. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein, and then ligated. The invention provides fusion proteins (see AAX32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components
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                                                                                                                                                                                                                                                                                                                                          New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
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                                                                                                          Tuberculosis, antigen; fusion protein; Mtb24; Ra12; DPPD; diagnosis; therapy; vaccine; immunogen; ss.
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                                                                                     Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                             Example, Fig 13A-B; 83pp; English.
                       AAZ20206 standard; DNA; 702 BP.
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                                                                                                                                                                                                            99WO-US007717
                                                                                                                                            Mycobacterium tuberculosis.
                                                                  (first entry)
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Best Local Similarity 100.
Matches 396; Conservative
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                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
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P-PSDB; AAY32071.
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30-DEC-1998;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycbacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cutantyport and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of sexum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                           360
                                                                                                                                                                              265 Arcaccedegregacececrecearcaacreeecacceceareecearescentare 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                                                                           GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence encoding Ral2-DPPD fusion protein.
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/*tag= a
/product= "Ral2-DPPD fusion protein"
                                                                                                                                                                                                                                                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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07-APR-1998;
30-DEC-1998;
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01-0CT-1997,
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/post; 263 . 265, as:Xaa / transl except = (pos:353 . 355, aa:Xaa) / transl except = (pos:454 / transl except = (pos:476 . 472, aa:Xaa) / transl except = (pos:470 . 472, aa:Xaa) / transl except = (pos:701 . 702, aa:Ser)
/partial except = (pos:701 . 702, aa:Ser)
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notes="No start or stop codon. Xaa= In frame stop codon"
2. .702
                                                                                                                                                                                  GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 240
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                                                           1 ACGCCCCCCCCCATAACTICCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 60
                                                                       145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACCAACGGCAACGGCACGA
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24.
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                    Length 702;
 Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
                    100.0%; Score 396; DB 4; Length 7
100.0%; Pred. No. 5.4e-84;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding antigenic fusion protein Ra12-DPPD (Mtb24)
                                                                                                                                                                                                                                                                                                        361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                          385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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partial
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/product= "Mtb24 #3"
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1. .702
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(first entry)
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                              Best Local Similarity 100.
Matches 396; Conservative
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08-MAY-2002
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis tuberculosis. This is equence represents DNA encoding an M. tuberculosis fusion protein of the invention. This polynucleotide encodes 3 different proteins, each in a different reading frame. (Updated on 29-AUG-2003 to standardise OS field)
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/note= "No start or stop codon"
/tranal_except= (pos:1. 2, aa:Pro) /tranal_except=
(pos:39. 41, aa:Xaa) /tranal_except= (pos:331. 323,
aa:Xaa) /transl_except= (pos:339. 341, aa:Xaa)
/tranal_except= (pos:339. 341, aa:Xaa)
/tranal_except= (pos:450. 452, aa:Xaa) /tranal_except=
(pos:621. 623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 ATCGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACGACAACGGCCAACGGCGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fusion proteins of Mycobacterium tuberculosis antigens, usef
diagnosing, treating or preventing M. tuberculosis infection,
particularly as vaccine for treating or preventing tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
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100.0%; Pred. No. 5.4e-84;
tive 0; Mismatches 0;
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P-PSDB; AAU74600, AAU76541, AAU76542.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
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Matches 396; Conservative
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
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us-09-684-215b-3.rng

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Best Local Similarity
Matches 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, or 6H polynucleotide, useful as vaccine to elicit protective immunity inst pathogenic microorganisms e.g. Leishmania and Mycobacterium
    300
                   GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCCAAGTCGGGCGGCGCCGCGT 360
                                                                                    384
                                                                                                                                                                                                                                                                                                                           Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; gene: antiden; ds.
    ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGGCGCG
                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Ra35FLMutSA mutant antigenic protein"
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                                                                                                                  ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 396
                                                                                                                                          ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 80-81; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                AAD47078 standard; DNA; 1002
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P-PSDB; AAE29703.
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                                                                                                                                                                                                                                                                                                                                             gene; antigen;
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100.0%; Score 396; DB 6; Length 1002;

Query Match

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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
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                                                                                                                                                                GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGT
                                                                                                                                                                                                                                           GOCCAGGCGATCGCCGCCCAGATCCGATCGGGTGGGGGGTCACCCATCAT
                                                                                                                                                                                                                                                                                                              658 dodcadoceandoceantecedoceaeceaenteceantecedoceaeceaeceaecearean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGCGACGCGT
                                                                                                 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                 Gaps
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/product="Ra35 mature antigenic protein"
/transl_except= (pos:547, .549, aa:Asp)
/transl_except= (pos:550, .552, aa:Ser)
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 993
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100.0%; Pred. No. 5.6e-84; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001; 2001US-0275837P
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                                     396; Conservative
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Disclosure; Page 79; 155pp; English.

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynuclectide sequence encoding an antigen or an antigenic fragment from Mycobaccerium sp. and a Leishmania polynuclectide sequence encoding a Delypeptide or ite fragment. The Leishmania polynuclectide is selected from TSA, LeIF, MIS, and 6H polynuclectides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as a vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobaccerium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynuclectides, as an in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mituberculosis mature Rais (N-terminus of MTB12A, RAISFE) antigen encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657
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; Pred. No. 5.6e-84;
0; Mismatches 0; Indels 0.
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Best Local Similarity 100.0%;
Matches 396; Conservative 0
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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 957

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Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB32A; Ra32FL; ss.
                                                                               Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA.
                                                                                                                                                                       /*tag= a
/product= "Ra35 mature protein"
/transl_except= (pos:547. .549, aa:Asp)
                                                                                                                                                   Location/Qualifiers
                     AAD28336 standard; cDNA; 1002 BP
                                                             (first entry)
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                                                                                                                                   Mycobacterium
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1 ACGCCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

Query Match
100.0%; Score 396; DB 6; Length 1002;
Best Local Similarity 100.0%; Pred. No. 5.6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0;

121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 718 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACAACGGCAACGG

120 717 180 777 240 837

9

Gaps 0 897 360

241 ATCACCGCGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300

838 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC

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GTCCAACGCGTGGTCGGGAAGCGCTCCGGCCAAGTCTCGGCATCTCCACCGGCGACGTG

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprositions comprositions antigens, nucleotides encoding them and particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serlogical sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammai, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as the munogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a CDNA encoding Mycobacterium species MTB32E) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
/transl_except= (pos:550. .552, aa:Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 95, 136pp, English.
                                                                                                                                    20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                              20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-147798/19.
P-PSDB; AAE17566.
                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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us-09-684-215D-5.rng

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Best Local Similarity 100.0%; Pred. No. 5.6e-84; Matches 396; Conservative 0; Mismatches 0;

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1 ACGGCCGCCGTCCCATTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the exclosical sensitivity of sera from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and insuling an immune response in a mammal, e.g., human, cuseful for eliciting an immune response in a mammal, e.g., human, mannish of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the population of Mycobacterium infection or monitoring of disease progression, as antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for rasing anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as avecines. Mrsalla sain proteins of the invention are also used as avecines of the invention are also used as a confice of fusion proteins of the invention are useful as in vivo diagnostic agents of the invention are useful as in vivo diagnostic agents of the intradermal skin test. The present sequence is a cDNA encoding Mycobacterium species RajzFL mature protein mutant, RajzFlMutSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
898 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 957
                                                                                                                                                                                                                                                                                                                                                                Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutein; ss.
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                                                                    958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 993
                                             361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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/*tag= a
/product= "Ra35FLMutSA protein"
                                                                                                                                                                                                                                                                                                                          Mycobacterium species Ra35FLMutSA mutant cDNA.
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                                                                                                                                                                                               AAD28337 standard; cDNA; 1002 BP.
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01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium sp.
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ID AAD
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DB 6; Length 1002;

100.0%; Score 396;

Query Match

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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
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                                                                                      240
                                                                                                          837
                                                                                                                               241 ATCACCGCGGTCGACGGCGCTCCGATCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                     717
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                                                            181 GTCCAACGCGTGGTCGGGGGGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                   GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                           121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species nucleic acid sequence 50D.
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P-PSDB; AAY05000.
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11-SEP-1997;
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detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                          790 ATCGGGCCTACCTCCTCGCTTGGGTGTTGTCGACAACAACGGCAACGGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                              970 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAACGAGTCGGGCGGCACGGT
                                                                                                                                           1 ACGGCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                 121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAGCGCAACGGCGCACGA
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Best Local Similarity 100.0%; Pred. No. 5.6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                         Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 U; 0 Other;
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P-PSDB; AAY04830.
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                                                                                                                       Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
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                                                                                                                                                                                                                                                                                                                                                        Sequence 1143 BP; 189 A; 373 C; 395 G; 186 T; 0 U; 0 Other;
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4. .1740
                                                             Claim 22; Fig 50F; 309pp; French
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (basion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (basion polypeptide) and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both a mantigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence
                                                                                                                                                                                                          Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 39pp; English
                  99US-0158585P
                                                                                                    Guderian
                                                                                                                                             WPI; 2001-266299/27.
P-PSDB; AAO22140.
                                                           (CORI-) CORIXA CORP
                    07-OCT-1999;
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Sequence 1742 BP; 372 A; 569 C; 490 G; 311 T; 0 U; 0 Other;

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Query Match 100.0%; Score 396; DB 4; Length 1742; Best Local Similarity 100.0%; Pred. No. 5.7e-84; Matches 396; Conservative 0; Mismatches 0; Indels 0;
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ADA26353 standard; DNA; 2181

RESULT 13 ADA26353

ADA26353

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, WTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antigens, with or without the WTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                     ds; gene; fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; WTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                                                                                                                                                                                              "MTB32-MTB39F fusion polypeptide'
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                                         Mycobacterium MTB32-MTB39F fusion protein encoding DNA
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100.0%; Score 396; DB 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-84;
Matches 396; Conservative 0; Mismatches 0;
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P-PSDB; ADA26354.
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                                                                                                                                    Mycobacterium sp.
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382 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 417
Query Match
100.0%; Score 396; DB 6;
Best Local Similarity 100.0%; Pred. No. 5.8e-84;
Matches 396; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
               GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                          Vaccine; immunity; diagnostic agent; gene therapy; TbH9; antigen; Ra35MutSA; Ra12; MTB72MutSA; chimeric; gene; ds.
                                                                                                                                                                                                                   Mycobacterium sp. MTB72FMutSA fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .2190
1. **Arg= a "MTB72FMutSA fusion protein"
/product= "MTB72FMutSA fusion protein"
                                                                ACAGGGAACGTGACATTGGCCGAGGGACCCCGGGCC 993
                                                  ACAGGGAACGIGACAITGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 92-93; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guderian J;
                                                                                                                                   AAD47084 standard; DNA; 2190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001; 2001US-0275837P
                                                                                                                                                                                                                                                                               Mycobacterium sp.
Mycobacterium tuberculosis.
                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-759844/82.
P-PSDB; AAE29709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                       WO200272792-A2
                                                                                                                                                                                  29-AUG-2003
27-JAN-2003
                                                                                                                                                            AAD47084;
                                                   361
                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                            RESULT 14
                                                                                                                                    Dp
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Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TbH9-Ra35MutSA; mutant; mutein; ds.
                                 Mycobacterium species MTB72FMutSA fusion protein encoding DNA.
                                                                              20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P
                                                                                                                                                                                                     20-JUN-2001; 2001WO-US019959
                       (first entry)
                                                                      Mycobacterium sp.
                                                                                                                                                                                WO200198460-A2
                                                                                                                                            misc_feature
                                                                                                          misc_feature
                                                                                                                           misc feature
                       22-APR-2002
                                                                                                                                                                                            27-DEC-2001
                                                                                                                                                              mutation
           AAD28343
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigento fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present equence is a nammal manale protein and Ralz protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise

BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

protein from Mycobacterium sp. field)

2190

Sequence

AAL40773 standard; DNA; 2191 BP.

AAL40773;

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the cuberculosis and methods for their use in diagnosis, prevention and readment of tuberculosis infection. Sequences of the invention and readment of tuberculosis infection. Sequences of the invention are useful for chiciting an immune response in a mammal, e.g., human, prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immuning on the constant of an infection are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MTB32R (Ral2-TDH9-Ra35MutSA) mutant fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GICCAACGCGIGGICGGGGGCGCICCGGCGCAAGICICGGCAICICCACCGGCGACGIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACCGCGGTCGACGCCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGTTAAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGGGCCTACCGCCTTCGCTTGGGTGTTGTCGACAACAACGGCAACGGCGACGCAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arceeeccraceeccrrcerecrreerrarierrereachacaacaaceaceecacacacaceacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                              Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGGCCGCGTCCCATTCCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ich 100.0%; Score 396; DB 6; Length 2190; al Similarity 100.0%; Pred. No. 5.8e-84; 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                                                                                                                          Claim 81; Page 108-109; 136pp; English.
                                                            Alderson M;
                    CORIXA CORP
                                                            Reed S,
                                                                                                    WPI; 2002-147798/19
P-PSDB; AAE17573.
                                                            Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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Best Local
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium imperculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCAGGCGATGGCGATCGGGATCCGATCGGGTGGGGGGGTCACCCATCGTTCAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (2) ATCGGGCCTACCGCCTTCGGCTTGGGTGTTGTCGACAACAACGGCAACGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                           Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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; Pred. No. 5.8e-84;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;
                                                                                                Nucleotide sequence encoding Ra12-H9-32A fusion protein.
                                                                                                                                                                                                                                                                                                        "Ral2-H9-32A fusion protein"
                                                                                                                                                                                                                                                 Location/Qualifiers
1. .2190
/*tag= a
/product= "Ral2-H9-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 396; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0158585P.
                                                                                                                                                                                                                                                                                                                                                                                                          36-OCT-2000; 2000WO-US027652.
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky Y, Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-266299/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                           WO200125401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1999;
                                                                                                                                                                                                    Unidentified
                                                                   03-OCT-2002
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                                                                                                                                                                                                                        Chimeric.
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RESULT 16 AAL40773

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particularly as vaccine for treating or preventing tuberculosis
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                          240
                                                                                          360
ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 300
                                                                    GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection,
                                    GICCAACGCGIGGICGGGAGCGCICCGGCGGCAAGICICGGCAICICCACCGGCGACGIG
                                                                                          GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
                                                                                                                                                                                                                                                          protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
ilostatic; immunogen; vaccine; Mtb32-Mtb39; Ral2; TbH9; Ra35;
                                                                                                                                                                                                                                           DNA encoding antigenic fusion protein Ra12-TbH9-Ra35 (Mtb32-Mtb39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-Neto
                                                                                                                                   ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                          ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alderson M,
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
42. .2231
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                                                                                                                                                                                   ABK14128 standard; DNA; 2286 BP
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97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
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                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-171134/22
P-PSDB; AAU74588.
                                                                                                                                                                                                                                                                                                                                                                                                     US2002009459-A1
                                                                                                                                                                                                                                                                            Ra12-TbH9-Ra35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
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08-MAY-2002
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            142
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(SKEI/)
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise os field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ATCACCGCGGGGGGGGGGGGTCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2286;
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2286 BP; 373 A; 719 C; 807 G; 381 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 396; DB 6;
100.0%; Pred. No. 5.8e-84;
tive 0; Mismatches 0;
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42. 2231
/*tag= a
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Example, Fig 1; 62pp; English
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Matches 396; Conservative
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 422
                                                                                                                                                                                                                                                                                                                                                  This DNA sequence includes a coding region for a recombinant Worobacterier Unberculosis tri-antigen fusion protein (see AAY12059), termed Mtb32A, composed of the antigens Ra12, TbH9 and Ra35. The DNA is useful for the recombinant production of the fusion protein. Coding acquences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. 3 Coding sequences for Ra12, TbH9 and Ra25 were ligated to encode Mtb32A. The invention provides fusion proteins (see AAY12059-T) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polywuclectides encoding them are useful as vaccines for preventing tuberculosis claimed. A for antigens of anti-with a sasays or intrademnal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 AceeccecerceannacriceAecierceAeereeccAeecnaeecAeenreeccArreecare
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                                                                                                                                                                                                                                                        New fusion proteins useful for diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogens than mixtures of the individual protein components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 396; DB 2; Length 2287; 100.0%; Pred. No. 5.8e-84; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2287 BP; 374 A; 723 C; 805 G; 382 T; 0 U; 3 Other;
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                                                                                                                                                            Campos-Neto A;
                                                                                                                                                                                                                                                                                                                  Example; Fig 1A-B; 83pp; English
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                    99WO-US007717
                                                          98US-00056556
                                                                             98US-00223040
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Matches 396; Conservative
                                                                                                                                                        Alderson M,
                                                                                                                                                                                             WPI; 1999-601610/51.
P-PSDB; AAY32059.
                                                                                                                  (CORI-) CORIXA
                                                                                                                                                                                                                                                                               tuberculosis
                    07-APR-1999;
                                                                             30-DEC-1998;
                                                          07-APR-1998;
                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leif, Mis, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a nimal. The invention is used in gene therapy. The present sequence is a nimal. The invention protein rule fusion protein comprises Rall and Rals protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATGGGGTGGGGGGGTCACCCGTTCAT 120
                                                                                                             diagnostic agent; gene therapy; TbH9; antigen; Ra35; pric; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                      Mycobacterium sp. MTB72F fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                     /product= "MTB72F fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 87-90; 155pp; English.
                                                                                                                                                                                                                                           Location/Qualifiers
42. .2231
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guderian J;
                                                                                                                                 chimeric; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                    Mycobacterium sp.
Mycobacterium tuberculosis.
Chimeric.
                  (revised)
(first entry)
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Best Local Similarity 100.
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky Y, Brannon M,
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P-PSDB; AAE29708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                               immunity;
                                                                                                                                                                                                                                                                                                                                            WO200272792-A2
                                                                                                                                 Ra12; MTB72F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis
                  29-AUG-2003
27-JAN-2003
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                                                                                                               Vaccine;
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182 180 242

AAD47083 standard; DNA; 2287 BP

AAD47083

AAD47083 ID AAD4 XX AC AAD4

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ATCACCGGGGTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGAGGCGCTTAAC 300
                                                                             GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGACGCGACGCGT 360
 240
          GTCCAACGCGTGGTTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTC 302
                                                                                                 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to fusion proteins containing at least tw Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase
                                                                                          363 GGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAACGAGGCGGCACGCGT
                                                                                                                                                                                                                                                                     Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72F; Ral2-TbH9-Ra35; ds.
                                                                                                                                                                                                                                                   Mycobacterium species MTB72F fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                                    Claim 62; Page 103-106; 136pp; English.
                                                                                                                                                                                        AAD28342 standard; DNA; 2287 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                                                               (first entry)
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P-PSDB; AAE17572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                     Mycobacterium sp.
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the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting uncoral infected with mycobacterium in ritro and in vivo assays for detecting in the intention of diagnosis of an infection or monitoring of disease progression, as intibodies or call-mediated immunity against M. tuberculosis for the diagnosis of an infection or monitoring of disease progression, as patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MIB32F (Ral2-TBH9-Ra35) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 396; DB 6; Length 2287; Best Local Similarity 100.0%; Pred. No. 5.8e-84; Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                          Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
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4. .2445
/*tag= a
/product= " MTB72F-DP
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Mycobacterium sp.
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                                                                                                                                                                                                                                       The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antiqen, or MTB2A, MTB32A and MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                            New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antiqens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                          18-FEB-2003; 2003WO-US004903
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396; Conservative
                                                                                                          Guderian J,
                                                                                                                               2003-697554/66.
                                                                                    CORIXA CORP
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WO2003070187-A2
                   28-AUG-2003
                                                                                                                                                                                                                    Claim 84;
                                                                                                          Skeiky Y,
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Matches
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                                              ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                               /product= "MTB72F-MTI (fusion MTB83F) protein"
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  protein encoding
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Pred. No. 5.9e-84;
o, Mismatches 0;
  (fusion MTB83F)
                                                                                                                                                                                              Location/Qualifiers
4. .2481
/*tag= a
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Best Local Similarity 100.
Matches 396; Conservative
Mycobacterium MTB72F-MTI
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P-PSDB; ADA26366.
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                                                                                                                                                     Mycobacterium sp.
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(first entry)

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ADA26359

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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucheotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucheotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, M15, and 6H polymucleotides. Sequences of the invention
                                                                                                                                                                                                                                  301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS
(aka r95f) fusion protein"
                                                                                                                                                    241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                 205 grecaaceceregreseaececreceseecesaagrereseearecaecaeceae
                                                                                                                                                                                  265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                           145 ATCGGCCTACCGCCTTCCTCGCTTGGGTGTTGTCGACAACAACAACAACGGCAACGA
                                                                           181 erccaaceceregeaececrecegeaecerecegeaeceaecere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA.
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                                                                                                                                                                                                                                                                                                               361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                       385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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P-PSDB; AAE29731.
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Leishmania sp.
Chimeric.
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27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or WTB32A, MTB32A mTB35A antigen. From a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
    GGGCATCATCCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 384
                                                                                                                                                                                                                                                                                                                                    ds, gene, fusion protein; MTB32A, MTB39; antigen; MTB32A; MTB35A, tuberculosis, tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACGCCCCCCCCCATAACTICCAGCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                 protein encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2637 BP; 428 A; 840 C; 928 G; 441 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
4. .2631
/*tea "MTB72F-Erd14 (fusion MTB89F)"
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0
                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 396; DB 8;
; Pred. No. 5.9e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 Mycobacterium MTB72F-Erd14 (fusion MTB89F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 84; Fig 6; 112pp; English.
                                                                                                                                                                                  ADA26358 standard; DNA; 2637 BP
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Best Local Similarity 100.0
Matches 396; Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky Y, Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-697554/66.
P-PSDB; ADA26365.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium sp.
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15-FEB-2002; 2002US-0357351P

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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGT 360
            useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymuclectides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. MTB72F Leishmania sp. thiol specific antioxidant (TSA; MTB72F (a 72 kDa poly-protein fusion construct comprises Mycobacterium sp. MTB72F (a 72 kDa poly-protein fusion construct comprising Ral2-TDH9-Ra35) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arcesecchaccecriccrcescrresererrereachacaachaceceacea 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265_ATCACCGGGTCGACGGCTCCGATCAACTCGGCCACGCGATGGCGACGCGTTAAC 324
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They are
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response in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                             Length 2808;
                                                                                                                                                                                                                                                                                                                                       Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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/*tag= a
/product= "MTB72F-MAPS (fusion r95F)"
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 396; DB 6;
100.0%; Pred. No. 5.9e-84;
tive 0; Mismatches 0;
   methods for eliciting immune
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Best Local Simil
Matches 396; C
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18-FEB-2003; 2003WO-US004903

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                                                                                                                                                                                                                                              The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB38 antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                          New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GICCAACGCGIGGICGGGAGCGCICCGGCGAAGICICGGCATCICCACCGGCGACGIG
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Best Local Similarity 100.0%; Pred. No. 5.9e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;
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                                                                                                                                                                                                                         Disclosure, Fig 5, 112pp; English
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                                                                     Reed
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                                                                                                                                                                                            tuberculosis infection.
                                                                      Guderian J,
                                                                                                   WPI; 2003-697554/66
                                         (CORI-) CORIXA CORP
                                                                                                                  P-PSDB; ADA26364.
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                                                                      Skeiky Y,
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955 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 990

BP

ADA26363 standard; DNA; 3060

RESULT 27

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(first entry)

20-NOV-2003

ADA26363;

product= "MTB-120F fusion protein" note= "No stop codon given"

2003WO-US004903 2002US-0357351P

Location/Qualifiers

1. .3030 /*tag= a /product= "

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Mycobacterium sp.
                   18-FEB-2003;
                     15-FEB-2002;
                28-AUG-2003
 Chimeric
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection. Claim 5; Fig 3; 112pp; English Reed Skeiky Y, Guderian J, WPI; 2003-697554/66. P-PSDB; ADA26356. (CORI-) CORIXA CORP

The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 annigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention. Sequence 3030 BP; 498 A; 966 C; 1062 G; 504 T; 0 U; 0 Other;

Claim 84; Fig 11; 112pp; English.

654 714 121 ATCGGGCCTACCGCCTTCCTCGGCTTGTGTCGACAACAACAACGGCACGACGA 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC Gaps ; Query Match
Best Local Similarity 100.0%; Pred. No. 6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 0

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ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 361

GOGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGCGCGCGT

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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                   ds, gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B.
                                                                                                                           Location/Qualifiers
4. 2054
/*tag= "MTB72F and 85b complex (fusion MTB103F)"
                                                 M. bovis MTB72F and 85b complex antigen (fusion MTB103F) DNA
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                                                                                                                                                                                                                                                                   Reed
                                                                                                                                                                                                                              15-FEB-2002; 2002US-0357351P
                                                                                                                                                                                                            18-FEB-2003; 2003WO-US004903
                                                                                                                                                                                                                                                                   Skeiky Y, Guderian J,
                                                                                                          Mycobacterium bovis.
                                                                                                                                                                                                                                                                                   WPI; 2003-697554/66.
P-PSDB; ADA26370.
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ö The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTBB5A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymeracicie of the invention may have a use in gene therapy, and as a polymeracic from a may have a use in gene therapy, and as a post of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention. The 144 Arcagaccraccaccrrcagcrragararraraacaacaacaacaacaacaa 180 204 84 25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGGATC 1 ACGGCCGCGTCCGATAACTTCCAAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC . 0 DB 8; Length 3060; Sequence 3060 BP; 503 A; 977 C; 1070 G; 510 T; 0 U; 0 Other; Query Match
Best Local Similarity 100.0%; Pred. No. 6e-84;
Matches 396; Conservative 0; Mismatches 0; Indels 61 121 145 19

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Gaps

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Indels

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Mismatches

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396; Conservative

Matches

9 84 180

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121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAAACGCCACGA

205 GICCAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCCGGCATCTCCACCGGCGACGTG 241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 265 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT

GICCAACGCGIGGICGGGGGGCGCTCCGGCGAAGICICGGCAICICCACCGGCGACGIG

181

120 144

61 GGCCAGGCGATGGCGATCGCGGGCCAGATCGGATCGGGTGGGGGGTCACCGTTCAT

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25 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTGCCCATTCGATC

1 ACGCCCCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

240

264 300 324 360

384

325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAAGTCGGGGGGACGGG

 36.1 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
 396

 38.5 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
 420

Mycobacterium MTB72F-mTCC#2 (fusion MTB114F) protein encoding DNA

(first entry)

20-NOV-2003

ADA26361

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ADA26361 standard; DNA; 3474

RESULT 2: ADA26361

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                                                                             GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
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                                                   New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infectios.
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               205 GICCAACGCGTGGGCGGAAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                     241 ATCACCGCGGTCGACGCCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
 GICCAACGCGICGGGGGCGCICCGGCGGCAAGICICGGCAICICCACCGGCGACGIG
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ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                                                                                                                           Location/Qualifiers
4. 23 48
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 84; Fig 9; 112pp; English
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P-PSDB; ADA26368.
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                                                                                                                       Mycobacterium sp.
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                                                                                                                                             Key
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

Claim 84; Fig 10; 112pp; English.

Score 396; DB 8; Length 3104; Pred. No. 6e-84;

100.0%;

Query Match Best Local Similarity

Sequence 3104 BP; 510 A; 968 C; 1104 G; 522 T; 0 U; 0 Other;

us-09-684-215b-3.rng

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              The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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ALIGNMENTS

| US-09-287-489-27|
| Sequence 27, Application US/09287449|
| Parent No. US20020009459A1
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| Parent No. US20020009459A1
| Parent No. US20020009459A1
| APPLICANT: Red Steven G. APPLICANT: Red Steven G. APPLICANT: Skeiky Ysair A.W. APPLICANT: Campos Neto, Antonio APPLICANT: Campos Neto, Antonio Protions of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: and Their Uses FILE REFRENCE: 014058-0092000 | TITLE OF INVENTION: and Their Uses FILE REFRENCE: 014058-0092000 | CURRENT FILING DATE: 1999-04-07 | PRIOR PLICATION NUMBER: US 08/918,112 | PRIOR APPLICATION NUMBER: US 08/918,112 | PRIOR APPLICATION NUMBER: US 08/918,12 | PRIOR PLICATION NUMBER: US 09/025,197 | PRIOR PELICATION NUMBER: US 09/025,197 | PRIOR PLICATION NUMBER: US 09/025,197 | PRIOR FILING DATE: 1998-02-18 | SOFTWARE: 1998-02-18 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO 27 | TITLE DATE: 1998-12-30 | TITLE DATE: 199

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Autonio
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
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          OTHER INFORMATION: bi-fusion protein Ra12-DPPD (designated Mtb24), OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame 2
NAME/KEY: CDS
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                                                                                                                                                                                                                                                Length 702;
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CTHER INFORMATION: reading frame 3
US-09-287-849-27
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Best Local Similarity 100.0
Matches 396; Conservative
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121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAAAAAGGGCAACGGCGCACGA 180
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Sequence 3, Application US/10098732A

Sequence 3, Application US/20030175294A1

PUBLICATION No. US20030175294A1

APPLICANT: Skeiky, Yasir

APPLICANT: Brainon, Mark

APPLICANT: Guderian, Jeffrey

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: US-012010US

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR APPLICATION NUMBER: US 60/275,837
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                                                         TYPE: DNA
ONGANISM: Artificial Sequence
PEATURE:
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein Ra12-DRPD (designated Mtb24), reading
OTHER INFORMATION: frame 1
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(693)
OTHER INFORMATION: bi-fusion protein Ra12-DPPD (designated Mtb24),
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Local Similarity 100.0%; Pred. No. 3e-107;
les 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(700)
OTHER INFORMATION: reading frame 2
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(701)
OTHER INFORMATION: reading frame 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 702
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241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCATCGCGGACGCGCTTAAC 300
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                                                                              GENERAL INCREMATION:
APPLICANT: Bisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-01-12
PRIOR PAPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
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100.0%; Score 396; DB 9;
Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 396; Conservative 0; Mismatches 0;
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US-09-712-363-15
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Patent No. US20020164588A1
GENERAL INFORMATION:
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US-10-098-732A-5

Sequence 5, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Goriza Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 014058-012010US
CURRENT FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 60/275,837

PRIOR PLILNG DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTHARE: Patentin Ver. 2.1

SEG ID NO 5

LENGTH: 1002
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                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature US-10-098-732A-3
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100.0%; Score 396; DB 15;
Best Local Similarity 100.0%; Pred. No. 3e-107;
Matches 396; Conservative 0; Mismatches 0;
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                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                          PatentIn Ver. 2.1
NUMBER OF SEQ ID NOS: 80
                  SOFTWARE: Pater
SEQ ID NO 3
LENGTH: 1002
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Qy 241 ATCACCGCGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300	ALCACCACAGE CARCAGES CONTROLLES C	Db 898 GGGCATCATCCCGGTGATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGC	928	KESULT / US-10-098-732A-17 ; Sequence 17, Application US/10098732A ; Publication No. US20030178294A1 ; CENEDRAL INFORMATION	JANEAL INCOMPATION YASIT APPLICANT: Skeiky, Yasir APPLICANT: Brannon, Mark APPLICANT: Gudarian, Jeffrey APPLICANT: Gudarian, Jeffrey	TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Leishmania Antigen ; FILE REFERENCE: 014058-012010US ; CURRENT APPLICATION NUMBER: US/10/098,732A	CURRENT FILING DATE: 2003-04-29 ; PRIOR APPLICATION NUMBER: US 60/275,837 ; PRIOR FILING DATE: 2001-03-13 ; NUMBER OF SEQ ID NOS: 80 ; SOFUMARR: Patentin Ver. 2.1 ; SEO ID NO 17	ficial Sequence	; OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA; OTHER INFORMATION: (Ra12-TbH9-Ra35MutSA) US-10-098-732A-17	Query Match 100.0%; Score 396; DB 15; Length 2190; Best Local Similarity 100.0%; Pred. No. 3e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 AGGCGGGTCCGATAACTICCAGCTGTCCCAGGGTGGGGATTCGCCATTCCGATC 60	Qy 61 GOGCAGCGATGGCGATCGCGGGCCAGATCCGATCGGTGGGGGTCACCCACC	ATGGGGCCTACCGCCTTCCTCGGCTTGGTCGACAACAACGGCAACGGCGACGA 		241	301 GGGATCATCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
	Oy 61 GGGCGATGGCGATGGCGGCCAGATCCGATCGGGGGGGGGG	Qy 121 ATGGGGCCTACGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 180 Db 790 ATCGGGCCTACCGCCTTCCTCGGCTTGTCGACAACGCCAACGGCGACGA 849	QY 181 GTCCAACGCGTGGTCGGAGGCGCTCCGGCGAAGTCTCCGCCATCTTCCACCGCGACGTG 240 Db 850 GTCCAACGCGTGGTCGGGAGGCCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 909	OY 241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300	Qy 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGCGCACGCGT 360	QV 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 396 Db 1030 ACAGGGAACGTGACCAAGGGACCCCCCGGCC 1065	RESULT 6 US-10-369-983-1 ; Sequence 1, Application US/10369983 ; Publication No. US20030235593A1	GARACAL INFORMATION: APPLICANT: Skeiky, Yasir APPLICANT: Skeiky, Jeff APPLICANT: Reed, Steven APPLICANT: Reed, Ste	APPLICANT: COLIXA COLPORATION: TITLE FOR INVENTION: Fusion Proteins of Mycobacterium Tuberculosis TITLE REPERENCE: 014058-009081US CURRENT APPLICATION NUMBER: US/10/369,983	CURRENT FILING DATE: 2003-02-18 ; PRIOR APPLICATION NUMBER: US 60/357,351 ; PRIOR FILING DATE: 2002-02-15 ; NUMBER OF SEQ ID NOS: 22	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 1 ; LENGTH: 2181 ; TYPE: DNA		US-10-369-983-1 Query Match	TCGATAACTTCCAGCTGCCCAGGTGGCAGGATTCGCCATTCCGATC 60	61 GGGCAGGCGATCGCGATCGGGCAGGTCGGATCGGGGTCGGGGTCACCCACC	Oy 121 ATCGGGCTACCGCCTTCGGCTTGGGTGTTGTCGACAACGACAACGGCGCACGA 180 12 ATCGGGCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCGCACGA 777	181 778

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361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCCGGCC 396
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| NAMENCEY: CDS
| LOCATION: (42)..(2231)
| FEATURE:
| NAMENCEY: modified_base
| LOCATION: (2270)
| OTHER INFORMATION: n = g, a, c or t
| US-10-359-460-1
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ORGANISM: Artificial Sequence
FEATURE:
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Sequence 1, Application US/09287849

Sequence 1, Application US/09287849

Sequence 1, Application US/09287849

Sequence No. US20020009459A1

GENERAL INFORMATION:

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: 1990-02108

FILE REFERENCE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/09/25,197

PRIOR PILING DATE: 1997-10-01

PRIOR PILING DATE: 1998-02-10

PRIOR PILING DATE: 1998-02-10

PRIOR PILING DATE: 1998-02-10

PRIOR PILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 1

LENGTH: 2287

TWPER DATE

LENGTH: 2287

TWPER DATE

LENGTH: 2287
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ra12-TbH9-Ra35 (designated Mtb32-Mtb39
OTHER INFORMATION: fusion)
NAME/KEY: modified_base
LOCATION: (30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 396; DB 9; Length 2287; Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n = g, a, c or t
NAWE/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42)...(2231)
NAME/KEY: modified_base
LOCATION: (2270)
LOCATION: (2270)
COTHER INFORMATION: n = g, a, c or t
US-09-287-849-1
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ORGANISM: Artificial Sequence
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RESULT 9
105-10-359-460-1
1 Sequence 1, Application Us/10359460
1 Publication No. US20030147911A1
1 GENERAL INFORMATION
1 APPLICANT: Reed, Steven G.
1 APPLICANT: Reed, Steven G.
2 APPLICANT: Reed, Steven G.
3 APPLICANT: Alderson, Mark
4 APPLICANT: Campos-Neto, Antonio
5 APPLICANT: Corina Corporation
7 TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
7 TITLE OF INVENTION: and Their Uses
7 TITLE OF INVENTION: and Their Uses
7 TITLE OF INVENTION: and Their Uses
7 TITLE OF INVENTION OF 1990-04-07
1 TITLE OF INVENTION NUMBER: US/09/287,849
1 PRIOR APPLICATION NUMBER: US 08/318,112
1 PRIOR FILING DATE: 1999-04-07
1 PRIOR FILING DATE: 1999-04-07
1 PRIOR FILING DATE: 1999-04-07
1 PRIOR APPLICATION NUMBER: US 08/325,197
1 PRIOR APPLICATION NUMBER: US 09/025,197
1 PRIOR FILING DATE: 1998-04-07
2 PRIOR FILING DATE: 1998-04-07
3 PRIOR FILING DATE: 1998-04-07
4 PRIOR FILING DATE: 1998-04-07
5 PRIOR PRIOR FILING DATE: 1998-04-07
5 PRIOR FILING DATE: 1998-04-07
5 PRIOR PRIOR FILING DATE: 1998-04-07
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NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
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Sequence 1, Application US/10359459;
Sequence 1, Application US/10359459;
Bublication No. US20040013677A1
GENERAL INFORMATION;
APPLICANT: Skeiky. Yasir
APPLICANT: Compos-Neto, Antonio
FILE REFERENCE: 014058-00901005;
CURRENT APPLICATION NUMBER: US/10/359,459
CURRENT APPLICATION NUMBER: US/10/359,459
FRIOR APPLICATION NUMBER: US/10/359,459
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
                                                      242
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                                                                                                                                                                                                                                                                                                                                              363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 422
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                                                    183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTTGTCGACAACAACAACAACGGCAACGGCAACGA
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 396; DB 16; Length 2287; Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
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NAME/KEX: modified_base

LOCATION: (30)

OTHER INFORMATION: n = g, a, c or t
FEATURE:

NAME/KEX: modified_base

LOCATION: (33)

OTHER INFORMATION: n = g, a, c or t
FEATURE:

NAME/KEX: modified_base

LOCATION: (42)...(2231)

FEATURE:

NAME/KEX: modified_base

LOCATION: (2270)

OTHER INFORMATION: n = g, a, c or t
OTHER INFORMATION: n = g, a, c or t
OTHER INFORMATION: n = g, a, c or t
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ORGANISM: Artificial Sequence
       121 ATCGGGCCTACCGCC
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US-10-359-459-1
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                                                                                                                          181 Grccaacecgregregeagecgrecegecegagecarcrecearcegegagege 240
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                                                                                                                                                                                                                                                                                                                                            303 ATCACCGCGGCGCGCGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 362
                                                                                                                                                                                                                                                                                                                                                                                           301 GGCCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCCACGCGT 360
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Sequence 15, Application US/20090175294A1
Sequence 15, Application No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Golderian, Jeffrey
APPLICANT: Golderian, Jeffrey
APPLICANT: Golderian, Jeffrey
FILE REFERENCE: 014058-01201001
FILE REFERENCE: 014058-01201001
FILE REFERENCE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 2287
TYPE: DNA
SORGANISM: Artificial Sequence
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FEATURE:
NAME/KEY: CDS
COCATION: (42)...(2231)
COTHER INFORMATION: MTB72F
FEATURE:
NAME/KEY: modified base
LOCATION: (1)...(2287)
COTHER INFORMATION: n = g, a, c or t
US-10-098-732A-15
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Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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61
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Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:fusion protein;
, OTHER INFORMATION: MTB81F (WTB72F-DPV)
US-10-369-983-8 RESULT 12
US-10-369-983-8
Sequence 8, Application US/10369983
Sequence 8, Application US/10369983
Sequence 8, Application No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Guderin, Jeff
APPLICANT: Guderin, Jeff
APPLICANT: Guderin, Jeff
APPLICANT: Greven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFREENCE: 014658-009081UG
FILE REFREENCE: 014658-009081UG
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
LENGTH: 2451 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 423 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 458 TYPE: DNA ORGANISM: Artificial Sequence 183 181 셤 a g 8 日 ò q ò ò g ò qq ò g à ò ò

241 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGACGCGCTTAAC 300

8 8

265 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGATGACGCGCTTAAC 324

SESSIGN OF SESSION OF	361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 	RESULT 13 US-10-369-983-7 Sequence 7, Application US/10369983 Publication No. US20030235593A1 GENERAL INFORMATION: APPLICANT: Skeiky, Yasir APPLICANT: Skeiky, Yasir APPLICANT: Guderian, Jeff APPLICANT: Green Steven TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis FILE REFRENCE: 014058-009081US CURRENT FILING DATE: 2003-02-18 FRIOR APPLICATION NUMBER: US/10/369,983 CURRENT FILING DATE: 2002-02-15 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: DESCRIPTION of Artificial Sequence:fusion protein US-10-369-983-7	Query Match Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ACGGCGCGTCCGATAACTTCCAGGTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 60	61 GGGCAGCCGATGGCGAGTCGCGGATCCGATCGGGTGGGGGTCACCCCACCGTTCAT 120	121 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACGGCAACGGCGCACGA 180	181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCAATCTCCACCGGCGACGTG 240	241 ATCACCGCGGTCGACGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300	301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGGTCGGGGGGGCGCGCTT 360 	361 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 396 	RESULT 14 US-10-369-983-6 1, Sequence 6, Application US/10369983 2, Publication No. US20030235593A1 3, GENERAL INFORMATION:
	e do	RESULT 13 US-10-369-983 Sequence 1, Sequence 1, SHOWING THE SECONT: APPLICANT: APPLICANT	Query Mat Best Loca Matches	& A	ò 8	29 29	Qy 1	oy oy	3 A	, qq	RESULT 14 US-10-369-5 ; Sequence ; Publicati ; GENERAL

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121 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACGGCAACGGCGCACGA 180
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ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence:WTB72F-WAPS

OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ra12-TbH9-Ra35)

OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ra12-TbH9-Ra35)

OTHER INFORMATION: (r85f) fusion construct, TB MTB72F (Ra12-TbH9-Ra35)

US-10-098-732A-64
                                                                                                                                                                                                                                                                                                           1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAATTCGCCATTCCGATC
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US-10-098-732A-64
Sequence 64, Application US/10098732A
Sequence 64, Application NG-102030175294A1
Sequence 64, Application NG-1020030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEC ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 ATCGGGCCTACCCCCGCTTGGCTTTGTGTTGTCGACAACAACGGCAACGGCGCACGA 204
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: WTB89F (MTB72F-Erd14)
US-10-369-983-6
  HAPPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
THILE OF INVESTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVESTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-09981US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LINNGTH: 2637
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100.0%; Score 396; DB 16; Length 2637;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
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Gaps
US-10-369-983-5

Sequence 5, Application US/1036983

Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Read, Steven
APPLICANT: Read, Steven
APPLICANT: Read, Steven
APPLICANT: Read, Steven
APPLICANT: Roles OF 1040981US
TITE REPERRICE: 014058-00981US
CURRENT FILING DATE: 2003-02-18
PRIOR PILICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2002-015
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PILING DATE: 2002-015
SOUTHARR: PATENTING DATE: 2002-015
SEQ ID NOS: 22

SEQ ID NO 5
IENGTH: 2808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence:fusion
) OTHER INFORMATION: R95F (MTB72F-MAPS)
US-10-369-983-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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100.0%; Score 396; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0;
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241 ATCACCGCGCTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                                                                                                               835 ATCACCCCGGTCGACGCCCCTTAACTCCGCCCACCGCGATGGCGGACGCGCTTAAC 894
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US-10-169-983-11
Sequence 11, Application US/10369983
Publication No. US20030235593A1
Publication No. US20030235593A1
Publication No. US20030235593A1
Publication No. US20030235593A1
Publication No. US2003023559A1
PAPLICANT: Graix Organia
APPLICANT: Graix Corporation
APPLICANT: Graix Corporation
APPLICANT: Gorix Corporation
APPLICANT: Graix Corporation
APPLICANT: Graix Corporation
APPLICANT: Gorix Corporation
APPLICANT: APPLICATION NUMBER: US/01/369, 983
CURRENT APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 3060
TABLE TO SET TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB103F (MTB72F-85b)
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100.0%; Score 396; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0;
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                                              25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCGGGTGGGCAGGGATTCGCCATTCCGATC 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10369983
; Sequence 3, Application US/10369983
; Publication No. USZ0030235593A1
; GENERAL INFORMATION:
    APPLICANT: Skeiky, Yasir
    APPLICANT: Reed, Steven
    APPLICANT: Reed, Steven
    APPLICANT: Corixa Corporation
    APPLICANT: Reed, Steven
    APPLICANT: Corixa Corporation
    APPLICANT: Corixa Corporation

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100.0%; Score 396; DB 16; Length
Best Local Similarity 100.0%; Pred. No. 3.1e-107;
Matches 396; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3030
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PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SCPTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 3474
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCription of Artificial Sequence:fusion protein
US-10-369-983-9

1 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGCTGGGCAGGGATTCGCCATTCCGATC Gaps ; 0 Length 3474; Indels Query Match 100.0%; Score 396; DB 16; Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0;

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: WTB102tm2F (WTB102FTM, MTB72F-hTCC#1)
US-10-369-983-10

TYPE: DNA ORGANISM: Artificial Sequence

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25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGAATTCGCCATTCCGATC 85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGTCCCCACCATCAT 121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCACGA

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205 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 145 ATCGGGCCTACCGCCTTCCTCGGCTTTGTCTGTCGACAACAACGGCGACGA 181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG g

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Query Match 100.0%; Score 396; DB 16; Best Local Similarity 100.0%; Pred. No. 3.1e-107; Matches 396; Conservative 0; Mismatches 0;

Length 3104;

ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCGCACGA 180

25 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 300 265 ATCACCGCGGTCGACGCCCCCGATCAACTCGGCCACCGCGCGATGGCGGACGGCGCTTAAC g ઠે

325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGGGCACGGT 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT g δ

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Sequence 4, Application US/10193002; Publication No. US20030135026A1; GENERAL INFORMATION: APPLICANT: Reed, Steven G. RESULT 21 US-10-193-002-4

Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Antonia
Houghton, Raymond
Vadvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND ME'

METHODS FOR

DIAGNOSIS

ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle CTATE: Washington COUNTRY: USA NUMBER OF SEQUENCES: 3:

ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALII

us-09-684-215b-3.rnpb

RESULT 19
US.10-369-983-10

Sequence 10. Application US/10369983

Sequence 10. Application US/10369983

Publication No. US2003023593A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff

APPLICANT: Reed, Steven

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFREENCE: 014658-009681US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 10

LENGTH: 3104

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GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240

205 GICCAACGCGIGGICGGGGGCTCCGGCGCGAAGICTCGGCAICTCCACCGGCGACGIG 264

145 Arceseceracescerrecresecrisserreresacaresacaresecaresecares

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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGCGGCACGCGT 384

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RESULT 20
US-10-369-983-9
Sequence 9, Application US/10369983
Sequence 9, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18

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191 GICCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCCACCGGCGACGTG 250
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NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STREET: 6300 Columbia Center, 701 Fifth Avenue
COMPUTER: 108A

EDENOMINER: 108A
COMPUTER: Floppy disk
COMPUTER: Flopp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: lines
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
US-10-098-732A-9
; Sequence 9, Application US/10098732A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 190
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US-10-084-843-4

i Sequence 4, Application US/10084843

i Sequence 5, Seven 6,

i Shelvan: Reed, Steven 6,

i Dillon, Davin C.

Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.

Twardik, Daniel R.

Lodes, Michael C.

i Lodes, Michael C.

Hendicken, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACGCCCCCCCCATCCTCCACCTCCCAGGTGGCCAGGATTCGCCATTCCGATC
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             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-701-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.6%; Score 394.4; DB 15;
Best Local Similarity 99.7%; Pred. No. 8.8e-107;
Matches 395; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | LENGTH 447 Dasse pairs | TYPE: nucleic acid | TYPE: nucleic acid | STRANDEDNESS: single | TOPOLOGY: linear | SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-193-002-4
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98.8%; Score 391.2; DB 15;
Best Local Similarity 99.2%; Pred. No. 7.9e-106;
Matches 393; Conservative 0; Mismatches 3;
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SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
US-10-084-843-17
Sequence 17, Application US/10084843
; Publication No. US20030143243A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-193-002-17
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian Jeffrey
APPLICANT: Guderian Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heishmania Antigen
FILE REBERERENCE: 014058-0120100S
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR PILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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OTHER INFORMATION: Description of Artificial Sequence: MTBRa12 (MTB32A)
OTHER INFORMATION: C-terminus)
US-10-098-732A-9
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 447;
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99.6%; Score 394.4; DB 15; Length
Best Local Similarity 99.7%; Pred. No. 8.8e-107;
Matches 395; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-193-002-17
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NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: LBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Uu1-2002
CLASSIFICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21,392
REFERENCE/DOCKET NUMBER: 21,132
REGISTRATION NUMBER: 31,332
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US-10-098-732A-1
| Sequence 1, Application US/10098732A
| Publication No. US20030175294A1
| Publication No. US20030175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Guderian, Jeffrey
| APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs
| TITLE OF INVENTION: Los Selected Fusion Protein Constructs
| TITLE OF INVENTION NUMBER: US 60/275,837 |
| PRIOR FILING DATE: 2001-03-13 |
| NUMBER OF SEQ ID NOS: 80 |
| SEQ ID NO 1 |
| LENGTH: 1872
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98.8%; Score 391.2; DB 15;
Best Local Similarity 99.2%; Pred. No. 7.9e-106;
Matches 393; Conservative 0; Mismatches 3;
                                                                                                      361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                           361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis PERATURE: OTHER INFORMATION: MTB32A (Ra35FL)
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CCATION: (1)...(1872)
OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1
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US-09-759-143-822
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                                                                                               Campos-Netco, Antonio
Campos-Netco, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
98.8%; Score 391.2; DB 15; Length 1872;
Best Local Similarity 99.2%; Pred. No. 7.9e-106;
Matches 393; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seartle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CONPUTE: 108A

ZONDUTE: 108A

APDIACATION TYPE: Floppy disk
COMPUTE: PATORI Release #1.0, Version #1.30

CURBUT APPLICATION NUMBER: US/09/072,967

FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/09/072,967

FILING DATE: 105-MAY-1998

ATTORINEY/AGENT INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-10-084-843-17
                                                          Skeiky, Yasir A.W.
Dillon, Davin C.
                                      Steven G.
              GENERAL INFORMATION:
APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   998
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190 GICCAACGCGTGGTCGGCGGGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 249
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Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Huual, John
APPLICANT: Huual, John
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REPERRNCE: 210.21.427024
CURRENT APPLICATION NUMBER: U$/09/780,669
CURRENT APPLICATION NUMBER: U$/09/780,669
CURRENT APPLICATION NUMBER: U$/09/780,669
CURRENT APPLICATION SPECIAL SECULIAR SECULI
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                                                                              Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
                            Harlocker, Susan L.
Jiang, Yuqui
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CORGANISM: Homo sapiens
US-09-780-669-822
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Best Local Similarity
Matches 379; Conserv
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Pred. No. 7.5e-95;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210.121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT APPLICATION UNDER: 20.1-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Sequence 822, Application US/09780669

Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
Sequence 822, Application US/09759143
Patent No. US20020022248Al
GENERAL INFORMATION:
                                                                                 Xi. Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 95.7%;
Matches 379; Conservative
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; ORGANISM: Homo sapiens
US-09-759-143-822
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240 189

81

Gaps

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Search completed: April 30, 2004, 07:45:33 Job time : 295 secs
                                                                                                                       TYPE: DNA
COGANISM: Homo sapiens
US-09-895-793-822
                                                                                                                                                                                                      Query Match
Best Local Simil
Matches 379; (
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                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGGCGATGGCGATCGCGGGCCAGATC-----AAGCTTCCAGGTTCAT 129
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Publication No. US2002019276341

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: March Michael D.

APPLICANT: State, March W.

APPLICANT: State, March W.

APPLICANT: Better, March W.

APPLICANT: Bay, Craig H.

APPLICANT: Day, Craig H.

APPLICANT: Li, Samuel X.

APPLICANT: Li, Samuel X.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Pranger, Gary R.

APPLICANT: Pranger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Panger, Gary R.

APPLICANT: Pranger, Gary R.

APPLICANT: Pranger, Gary R.

APPLICANT: Pranger, Gary R.

APPLICANT: Pranger, Gary R.

APPLICANT: Panger, Gary R.
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                                                                                                                                                                                                      Score 354; DB 9; Length 675;
Pred. No. 7.5e-95;
0; Mismatches 5; Indels
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CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ TUDNO 822
LENGTH: 675
                                                                                                                                                                                                             Query Match
Best Local Similarity 95.7%;
Matches 379; Conservative
                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-822-827-822
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US-09-895-793-822
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                                                                                                                                                                                                                                           Similarity 95.7%; Pred. No. 7.5e-95; Conservative 0; Mismatches 5
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 675
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Sequence 27, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 17, Appli
Sequence 182, Appli
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Sequence 182, Appli
Sequence 1861, Appli
Sequence 353, Appli
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Sequence 353, Appli
Sequence 354, Appli
Sequence 351, Appli
                                                                  April 30, 2004, 05:13:09; Search time 64 Seconds (without alignments) 3433.759 Million cell updates/sec
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                                                                                                              US-09-684-215B-3
396
1 acggccgcgtccgataactt......tggccgagggacccccggcc 396
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2: /ogn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /ogn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /ogn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /ogn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /ogn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-736-457-1861
US-09-643-597-351
US-09-604-21B-351
US-09-685-166A-851
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                                                                                                                                                                                             682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
                                                                                                                                                          IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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354 89.4 1464 4 US-09-520 354 89.4 1557 4 US-09-520 354 89.4 1557 4 US-09-598 354 89.4 1557 4 US-09-598 354 89.4 1578 4 US-09-556 354 89.4 1578 4 US-09-556 354 89.4 1752 4 US-09-598 354 89.4 1752 4 US-09-598 354 89.4 1758 4 US-09-598 354 89.4 1860 4 US-09-598 354 89.4 1941 4 US-09-598 354 89.4 1941 4 US-09-598 354 89.4 1941 4 US-09-598	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
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	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

NESULT 1  OB-09-287-849-27  Sequence 27 Application US/09287849  Patent No. 6627198  GENERAL INFORMATION: APPLICANT: Skelky, Yasia A.W. APPLICANT: Skelky, Yasia A.W. APPLICANT: Campos-Neto, Antonio TITLE OF INVENTION: Fusion Protiens of M TITLE OF INVENTION: Rusion Protiens of M TITLE OF INVENTION: By 1990-00-00  TITLE OF INVENTION: 1997-00-01 PRIOR PRILING DATE: 1999-04-07 PRIOR FILING DATE: 1998-02-18 PRIOR PRILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18 PRIO	949-27  2. Application US/09287849  2. 6627198  WRITE Read, Steven G. WRITE Skelky, Yasir A.W. WRITE Dillon, Davin C. WRITE Carbon, Davin C. WRITE Carbon, Davin C. WRITE Carbon, March C. WRITE Carbon, WARRER US 08/942,578  FILING DATE: 1999-04-07  PRILING DATE: 1999-04-07  PRILING DATE: 1999-04-07  PRILING DATE: 1998-02-18  PRILING DATE: 1998-02-18  PRILING DATE: 1998-02-18  PRILING DATE: 1998-02-18  WRITE CARBON NUMBER: US 09/025,97  PRILING DATE: 1998-04-07  PRILI
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63 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 122 181 g 유 엄 8 8  $\delta$ ద ઠે 8 181 GICCAACGCGIGGICGGGAGCGCICCGGCGCAAGICICGGCAICICCACCGGCGACGIG 240 241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 300 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360 121 ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACGGCGCACGA 180 145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 204 205 Greenacedescencesasesceredesceseseasereresseareredescences 264 265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC 324 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 384 1 ACGCCCGCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 60 25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC Gaps ö 0; Indels 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 385 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 420 0; Mismatches 396; Conservative Matches 셤 셤 g qq Q Dp ð ò ò à à

REBUIT 2
US-09-223-040-1
Sequence 1, Application US/09223040
Patent No. 6544520.
Patent No. 6544520.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Nec

Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-95;
Matches 396; Conservative 0; Mismatches 0; Indels 0;

1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC

Sequence 1 Application US/09287849

| Sequence 1 Application US/09287849
| Pacent No. 6627198
| GERERAL INFORMATION:
| APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Vasir A.W. APPLICANT: Skeiky, Mark APPLICANT: Campoe-Neco, Antonio APPLICANT: 1999-04-07
| TITLE OF INVENTION: 1999-04-07
| TITLE OF INVENTION UNMERR: US 08/281,12
| PRIOR APPLICATION NUMBER: US 08/223,040
| PRIOR APPLICATION NUMBER: US 09/223,040
| PRIOR APPLICATION NUMBER: US 09/223,040 183 ATCGGGCCTACCCCCTTCCTCGGCTTTGGCTGTTGTCGACAACGGCAACGGCGCACGA 242 Grecaacdecardedaccerrececcaccaacterrececcarerececcaccare 240 243 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 302 241 ATCACCGCGGTCGACGCCCTCCGATCACTCGGCCACGCGGATGGCGGACGCGCTTAAC 300 303 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 362 363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGGCACGCGT 422 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 360 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396

CTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)

NAME/KFS: modified_base

LOCATION: (30)

OTHER INFORMATION: n = g, a, c or t

NAME/KFS: modified_base

LOCATION: (33)

OTHER INFORMATION: n = g, a, c or t

NAME/KFS: CS

LOCATION: (42):.(2231)

NAME/KFS: modified_base

LOCATION: (2201)

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Patent No. 6294328

GENERAL INFORMATION

APPLICANT: FLEISCHAAN, Robert D.

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-2007.00

CURRENT APPLICANTON NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENTH: 4403765

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FRAURE:
FRA 9 151984 ACGGCGCGCTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCAATCGATC 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC GGGCAGGCGATGGCGACCCAGATCCGATCGGGTGGGGGGCTCACGGTTCAT 183 ATCGGGCCTACCGCCTTCTCGCGCTTGGGTGTTGTCGACAACAACAACGGCACGA ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCGATTCCGATC Grecaaccegregerecegrecrecegecaccaaccegearereceaccaccegecaacce 1 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC Gaps Gaps Query Match 100.0%; Score 396; DB 3; Length 4403765; Best Local Similarity 100.0%; Pred. No. 2.1e-94; Matches 396; Conservative 0; Mismatches 0; Indels 0; . 0 Length 2287; OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout OTHER INFORMATION: represent a, t, c or g 0; Indels ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458 Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-95;
Matches 396; Conservative 0; Mismatches 0; ö U ď Ď u c ; OTHER INFORMATION: US-09-287-849-1 RESULT 4 US-09-103-840A-2 61 241 303 423 361 301 63 19 123 121 181 243 d g à  $\dot{\delta}$ Db 셤 g ò ò

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                                                                                                                                                        241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGGATGGCGGACGCGCTTAAC
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                                                    GTCCAACGCGTGGGGGGGGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
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100.0%; Score 396; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.1e-94;
Matches 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHAM, Robert D.
APPLICANT: FLEISCHAM, Robert D.
APPLICANT: FRAER, Claire M.
APPLICANT: FRAER, Claire M.
TITLE OF INVENTION: John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 2436-21007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTING UNCE: 2.1
SEQ ID NO!
LENGTHAM 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORCANISM: Mycobacterium tuberculosis
; CTHER INFORMATION: H37Rv
US-09-103-840A-1
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251 ATCACCGCGCGCGCGCGCCCCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310 311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAAACCAAGTCGGGCGGCACGCGT 370 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 용 강 쉱 셤 à 71 GGGCAGGCGATGCCGGGCCCAGATCCGATCGGGTGGGGGGTCACCCATCAT 130 121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAAACGGCGCACGA 180 181 Grccaacgegregregagegetecgecgecageaagreregearterecaceacgacgreg 240 241 ATCACCGGGTCGACGGGGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 300 1 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 60 Gapa Sequence 4 Application US/08818112
Patent No. 6290869

Patent No. 6290869

Patent No. 6290869

Patent No. 6290869

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.

PAPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Wardzik, Daniel R.

APPLICANT: Wardzik, Daniel R.

CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 1330
CONTURN: USA

CONTURN: USA

CONTURN: USA

CONTURN: USA

CONTURN: DANIE: 13-MAR-1997

CASSIFICATION NUMBER: 21012.411C6

FELECOMMUNICATION NUMBER: 21012.411C6

TELESPANE: (206) 622-4900

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH 447 base paire
TYPE: nucleic acid
TYPE: nucleic acid . 0 Query Match 99.6%; Score 394.4; DB 3; Length 447; Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels 0; 152175 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 152210 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 ; TOPOLOGY: linear US-08-818-112-4 d 셤 ò ዊ ያ q ò dd ò

RESULT 7 US-08-818-111 Sequence 4, Patent No., GENERAL IN APPLICAN	-4 Application U 633865 FORMATION: T: Reed, Stev T: Skeiky, Ye T: Dillon, Da T: Campos-Net T: Houghton,
APPLI	Twardzik, Daniel NVENTION: COMPOUN SEQUENCES: 148
ST.	RRESPONDENCE ADDRESS: ADDRESSEBE: SBED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
	CITY: Seattle STATE: Washington COUNTRY: USA
; COMF	104-7092 EADABLE FORM:
	MEDIUM TYPE: Floppy disk COMPUTER: IBM FC comparable ORDSAMTHA GYGNEW. DATACKALIDG
SS	u :
, AE	ARENI AFFILOTION VOMBER: US/08/818,111 APPILOTION VUMBER: US/08/818,111 FILING DATE: 13-MAR-1997
, ATTC	AGENT I
N N N	NAME: Maki, David J. SEGISTRATION NUMBER: 31,392 DEBEDERATE ADARGE 310131 41705
TELE	ION:
; TELEFHOR ; TELEFAX: ; INFORMATION	E: (206) (206) 68 FOR SEO II
SEOT	HARACTER 447 bas
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	STERNINGIELC ACID STRANDENESS: single TOPOLOGY: linear 18-111-4
Query M Best Lo Matches	Query Match Best Local Similarity 99.6%; Score 394.4; DB 4; Length 447; Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ò	1 ACGCCCGGTCCGATAACTTCCAGCTGTCCCAGGGGTGGGCAGGGATTCGCCATTCCGATC 60
qq	11 ACGGCCCCGTCCGATAACTTCCAGCTGCCGAGGGGGGGGG
à	61 GGGCAGCGATGGCGGGCCAGATCCGATCGGGTGGGGGGGTCACCGTTCAT 120
qq	71 GGGCGAGGCGATGGCGATCGCGAGGCCAGATCGGGTGGGGGGGG
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qq	131 Arcadaccialaccaccricarcadariandarianda (Arcadaca Arcadaca (Arcadaca Arcadaca Arc
ζŏ	181 GICCAACGCGIGGICGGGAGCGCICCGGCGAAGICTCGGCAICTCCACCGGCGACGIG 240

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181 GTCCAACGCTGGGAGCGCTCCGGCGGCAAGTCTCCGCCGGCGACGTG 240   181 GTCCAACGCTGGTCGGCGAAGTCTCGGCAATCTCCACCGGCGACGTG 240   191 GTCCAACGCTGGTCGCGACGCGCCAACGCGCGAAGTCTCCGGCATCTCCACCGGCGACGTG 250   241 ATCACCGCGTGGTCGCGCGTCCCCAACACTCGGCCACCGCGATGACGCGCTTAAC 300   251 ATCACCGCGGTCGACGCGTCCCGATCACTCGGCCACCGCGATGACGCGCTTAAC 310   1	RESULT 9  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-4  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-072-596-6  18-09-07-07-07-07-07-07-07-07-07-07-07-07-07-	DENGTH: A47 base pairs  TYPE: nucleic acid  TYPE: nucleic acid  TYPE: nucleic acid  STRANDEDNESS: single  TYPE: nucleic acid  STRANDEDNESS: single  TYPE: nucleic acid  STRANDEDNESS: single  STRANDED
	on US/09056556  teeven G.  Yasir A.W. Davin C. COMPOUNDS AND METHODS FOR THE PREVENTION AND SES: and BERRY LLP umbia Center, 701 Fifth Avenue  TO Compatible Compatible Compatible Compatible FO-DOS/MS-DOS IN Release #1.0, Version #1.30 IN Rolease #1.0, Version #1.30 RRPR-1998	5=5 8=8 5=5

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                                                                                                                 1 ACGCCCCCCCCCATAACTTCCAGCTGTCCCAGGCTGGGCAGGATTCGCCATTCCGATC
                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos Meto, Antonio
APPLICANT: Campos Meto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Varidaik, Thomas S.
APPLICANT: Varidaik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
Best Local Similarity 99.7%; Pred. No. 7.6e-95; Matches 395; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: WEALTH HEALTH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1872 base pairs
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   GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCTTCAT 130
                                                                                                                                                                GICCAACGCGIGGICGGAGCGCICCGGCGGCAAGICTCGGCAICTCCACCGGCGACGIG 240
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Sequence 4, Application US/09072967

Sequence 4, Application US/09072967

Sequence 4, Application US/09072967

GENERAL INCOMMATION:

APPLICANT: Read, Steven G.

APPLICANT: Campos Neto, Autonio

APPLICANT: Campos Neto, Autonio

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Hendrickeon, Romaid C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS OF TUBERCULOSIS

NUMBER OF SEQUENCE: 355

ADDRESSEE: SEED and BERRY LLP

STREET: Seattle

COMPUTER: Seattle

COMPUTER: Seattle

COMPUTER: IMP PC compatible

COMPUTER: IMP PC compatible

COMPUTER: The PC compatible

COMPUTER: The PC compatible

COMPUTER: The PC compatible

COMPUTER: The PC compatible

COMPUTER: DATE: OF-NAY-1998

CLASSIFICATION NUMBER: 31,392

CLASSIFICATION NUMBER: 31,392

RESTREMENDED/DOCKET NUMBER: 210121.411C9

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: READ-TRICATION: NUMBER: 210121.411C9

TELEPHONE: (206) 622-4900

INFORMATION FOR SEQ ID NO: 41

SEQUENCE CHARACTERISTICS:

LENGTH: 447 has naive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 447;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-072-967-4
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RESULT 13
US-09-056-556-17
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Sequence 17, Application US/08818111

Patent No. 633852

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Twardzik, Daniel R.
APPLICANT: Sactle Conter, 701 Fifth Avenue
CITY: Seattle Sactle Columbia Center, 701 Fifth Avenue
CITY: Seattle Sactle R.
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INPORMATION:
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INPORMATION:
                                                                                          Length 1872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                    Query Match
Best Local Similarity 99.2%; Pred. No. 7.2e-94;
Matches 393; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
; TYPE: nucleic acid
; STRANDEDNES: single
; TOPOLOGY: linear
US-08-818-112-17
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US-08-818-111-17
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Sequence 17, Application US/09056556

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Scalt, No.
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSES: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
COUNTRY: USA
COMPUTER: IBM PC compatible
SIATE: PORDELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US-DARMATION:
APPLICATION DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GGGCATCATCCCGGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACGGCCGCGTCCGATAACTTCCAGGTGCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                               98.8%; Score 391.2; DB 4; Length 1872; 99.2%; Pred. No. 7.2e-94; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ACAGGGAACGTGACATTGGCCGAGGACCCCCGGCC 396
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NAME: Maki, David 0.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-17
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.2
Matches 393; Conservative
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us-09-684-215b-3.rni

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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
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; Sequence 17, Application US/09072967
; Patent No. 6592877
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CITY: Seattle
STATE: Washington
                           FILING DATE: 0
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                      linear
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US-09-056-556-17
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APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Todes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: APPLICANT: NOT SEQUENCES: 355
CORRESPONDENCES: 355
CORRESPONDENCES: 355
ADDRESSEE: SEED and BERRY LLP
APPLICANT: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCES: 355
CORRESPONDENCES: 355
ADDRESSEE: SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGIGTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121,417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6930
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1057

937 240

877

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61 GGGCAGGCGATGGCGGGCCAGATGCGATCGGGTGGGGGGGTCACCCAACCGTTCAT 120
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APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedyick, Thomas S.
APPLICANT: Vedyick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Aliun
APPLICANT: Repler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 822
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-822
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98.8%; Score 391.2; DB 4; Length 1872;
Best Local Similarity 99.2%; Pred. No. 7.2e-94;
Matches 393; Conservative 0; Mismatches 3; Indels 0;
COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
TYPE: nucleic acid
STRANDBDNESS: single
TOPOLOGY: linear
COMPUTED ASSIGNED INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
TYPE: nucleic acid
STRANDBDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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THE THERAPY AND

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US-0-689-165A-826.
Sequence 822, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hardocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ranger, Gary R.
APPLICANT: Renger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Oay, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
RESULT 17
US-09-685-166A-822
```

Sequence 822, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.

RESULT 16 US-09-636-215-822

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us-09-684-715D-3.ru1
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#007 co:0c:0c c

MOII May

MENUL: 19

GENERAL INCRAMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liquum

APPLICANT: Alos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: APPLICANT: Anney

APPLICANT: Banger, Gary R.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Mang, Aljun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Bangur, Compositions And Diadrosis OF LUNG CANCER

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: COMPOSITIONS AND CONFOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: COMPOSITIONS AND SECTION OF SECTI 370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-736-457-1862 ઠે à 유 ð g à à 유 à ઠે 121 ATCGGGCCTACCGCCTTCCTCGGCTTGGTTGTCGACAACAACGGCAACGGCGCACGA 180 130 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACAACGGCGACGA 189 181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 240 190 GTCCAACGCGTGGTCGCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 249 250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGACGCGCTTAAC 309 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACCGT 360 241 ATCACCGCGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 1 ACGCCCCCCCATAACTICCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 60 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCGGGTGGGCAGGGATTCGCCATTCCGATC 81 Gaps Query Match
89.4%; Score 354; DB 4; Length 675;
Best Local Similarity 95.7%; Pred. No. 3.4e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 12; THE THERAPY AND APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-110-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675 Sequence 1862, Application US/09736457

Patent No. 6509448

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Eanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Fanger, March
APPLICANT: Retter, Darrick
APPLICANT: Retter, March
APPLICANT: Retter, March
APPLICANT: Retter, March
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, 190000111000 AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOUTHWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1822 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 370 ACAGGAACGTGACATTGGCCGAGGACCCCCGGCC 405 TYPE: DNA
CRGANISM: Homo sapiens
US-09-685-166A-822 RESULT 18 US-09-736-457-1862 301 ద à g ð a à g à d ò 셤 ò

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249
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22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                          22 ACGGCCGCCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                       181 GICCAACGCGIGGICGGGAGCGCTCCGGCGGCAAGICICGGCAICICCACCGGCGACGIG
                                                                                                         1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                    Gaps
                                                       12;
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     Length 822
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Query Match

89.4%; Score 354; DB 4; Length 82:
Best Local Similarity 95.7%; Pred. No. 3.5e-84;
Matches 379; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 89.4%; Score 354; DB 4; Length 90 Best Local Similarity 95.7%; Pred. No. 3.6e-84; Matches 379; Conservative 0; Mismatches 5; Indels
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309 360 369

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61 GGGCAGGCGATGGCGAGTCGCGAGATCCGATCGGGTGGGGGGTCACCCGTTCAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACGGCCGCGTCCCGATAACTTCCAGCTGCCAGGGTGGCCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGGCAACGGCGCAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GICCAACGCGIGGICGGAAGCGCICCGGCGCAAGICICGGCAICTCCACCGGCGACGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                     310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Au, tatawara.

APPLICANT: Dillon, Davin.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Senger, Gary R.

APPLICANT: State H.

APPLICANT: Carter, Day, Craig H.

APPLICANT: Carter, Day, Craig H.

APPLICANT: Day, Craig H.

APPLICANT: Wang, Aijun

APPLICANT: Day, Seiky, Yasuel

APPLICANT: Wang, Aijun

APPLICANT: Day, Craig H.

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Bepler, William

TITLE OF INVENTION: DIAGONS OF PROSTATE CANCER

FILE REFERENCE: 210121.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARET FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARET FILING DATE: LENGER

BENGTH: 915

LENGTH: 915
241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCCGATGGCGGACGCGCTTAAC
                        250 ATCACCGGGGTCGACGGCGCTCCGATCAACTCGGCCACGGGATGGCGGACGCGCTTAAC
                                                                                      301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.4%; Score 354; DB 4; Length 915;
Best Local Similarity 95.7%; Pred. No. 3.6e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 915;
                                                                                                                                                                            361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                       370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                           REGULT 21
US-09-636-215-834
US-09-636-215-834
Sequence 834, Application US/09636215
Patent No. 6620822
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                  Xi. Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Ralos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-636-215-834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GTCCAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
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                                                                                                              180
                                                                                                                                        130 ATCGGGCCTACCGCCTTCCTCGGCTGTGTCGCGACAACGGCAACGGCGCACGA 189
                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                        250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGAACGTTAAC 309
                                                                                                                                                                                                                                                                                                                                                                                 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGCGCACGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                   310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGT 369
                                                                                                                                                                                                                                                190 GTCCAACGCGTGGTGGGGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 249
                                                                                                                                                                                                                                                                                             241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                        22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACGGCCGCGTCCGATAACTTCCAGCTGCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGGCGCCACGA
                                                              GGGCAGGCGATGGCGATCGCCGGCCAGATC------AAGCTTCCCACGTTCAT
                                                                                                              ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                    GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 353, Application US/09606421B

Farent No. 6531315

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Hosken, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
ITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
ILLE REPERBANCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 353
LENGTH: 900

"LENGTH: 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-09-606-421B-353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAACGCGCTTAAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 descadescarrescarresceses es anticolo de contra de co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GICCAACGCGTGGTCGGGAAGCCTCCGGCGGCAAGICTCGGCATCTCCACCGGCGACGTG
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Panger, Gary
APPLICANT: Reter, Darrick
APPLICANT: Reter, Mannion, Jane
APPLICANT: Reter, Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
APPLICANT: Wan
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89.4%; Score 354; DB 4; Lv
Best Local Similarity 95.7%; Pred. No. 3.7e-84;
Matches 379; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 Acadedaacercacarredeceaacececedeec 405
370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                            Sequence 1861, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 351, Application US/09643597; Patent No. 6426072
Patent No. 6426072
PAPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ran, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-736-457-1861
                                                                                                                                                                        JS-09-736-457-1861
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US-09-643-597-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ATCGGGCCTACCGCCTTCGGCTTGGGTGTTGTCGACAACAACGACAACAACGGCGCACGA 189
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
FILE REFERENCE: 210121-427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
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                                                                                                                                     361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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89.4%; Score 354; DB 4;
Best Local Similarity 95.7%; Pred. No. 3.6e-84;
Matches 379; Conservative 0; Mismatches 5
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 834, Application US/09685166A Patent No. 6630305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, bavin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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CORGANISM: Homo sapiens
US-09-685-166A-834
                                                                                                                                                                                                                                                                                                                                        RESULT 22
US-09-685-166A-834
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241 ATCACCGCGGCGCTCCGATCCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE RPERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                      12;
                             Length 1012;
Score 354; DB 4; Length 10:
Pred. No. 3.7e-84;
0; Mismatches 5; Indels
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JS-09-636-215-851

61 Н සු දු 성 음 q ò g ઠે ò 8 8 8 B 8 원 상 원 \$ 8 \$ ď g GICCAACGCGIGGICGGGGGGCTCCGGCGGCAAGICTCCGGCATCTCCACCGGCGACGTG 110 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGCGCACGCGT 369 82 GGGCAGGCGATGGCGATCGCGGGCCAGATC-----AAGCTTCCCACGTTCAT 129 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAAACGGCGCACGA 180 GICCAACGCGIGGICGGAGCGCICCGGCGGCAAGICICGGCAICICCACCGGCGACGIG 240 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300 250 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 309 GGGCATCATCCCGGGGGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 360 81 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCAGGGATTCGCCATTCCGATC Gabs 12; THE THERAPY AND Query Match

89.4%; Score 354; DB 4; Length 1203;
Best Local Similarity 95.7%; Pred. No. 3.8e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 1: Length 1203; Query Match 89.4%; Score 354; DB 4; Length 12 Best Local Similarity 95.7%; Pred. No. 3.8e-84; Matches 379; Conservative 0; Mismatches 5; Indels US-09-685-166A-851
US-09-685-166A-851
Sequence 851, Application US/09685166A
Sequence 851, Application US/09685166A
Setent No. 6630305
GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ratos, Michael D.
APPLICANT: Retter, March W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Wasir A.W.
APPLICANT: BERERENCE: 2101214,427C1
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: EERSENCE FOR Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396 TYPE: DNA ORGANISM: Homo sapiens ús-09-685-166A-85 130 121 181 190 241 301 \$ B \$ B \$ 셤 ò 원 g 8 g ò

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120 129 180 189 240 249 300 309 129 180 189 240 249 300 309 360 369 120 9 81 9 8 22 ACGGCCGCGCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCCATC 190 GICCAACGCGIGGTCGGAAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG ATCACCGCGGTCGACGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 82 GGGCAGGCGATGGCGATCGCGGGCCAGATC-----AAGCTTCCCACCGTTCAT 121 ATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 181 GICCAACGCGIGGICGCGCGCGCGCGCGCAAGICTCGGCAICTCCACCGGCGACGIG 241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 82 GGGCAGGCGATGCCGGGCCCAGATC------AAGCTTCCCACGTTCAT 121 ATCGGGCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACAACGACGCGCACGA 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT 310 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGT 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTGGGCAGGGATTCGCCATTCCGATC ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 12; AND Query Match

89.4%; Score 354; DB 4; Length 1464;
Best Local Similarity 95.7%; Pred. No. 4e-84;
Matches 379; Conservative 0; Mismatches 5; Indels 1 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGCC 396 370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC ; TYPE: DNA ; ORGANISM: Chlamydia trachomatis US-09-620-412C-348 -09-620-412C-348 241 250 a

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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGT 360
                                                  GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGT 369
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Pred. No. 4e-84;
0; Mismatches 5; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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                                                                                                                                                                ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Patent No. 6448234
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REPERENCE: 210121.4697.
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-598-419-348
. Sequence 348, Application US/09598419
. Patent No. 6565856
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.7%;
Matches 379; Conservative
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US-09-620-412C-332
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NUMBER OF SEQ ID NOS: 363 SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 3322 LENGTH: 1557

; TYPE: DNA ; ORGANISM: Chlymadia trachomatis US-09-620-412C-332

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
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-NO MARP -LARGEGUERY -NEG-SCORE=s0 -MAIT -DSPBICK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 April 29, 2004, 22:25:27; Search time 2585.37 Seconds (without alignments) 1524.660 Million cell updates/sec US-09-684-215B-4 675 1 TAASDNFQLSQGGGGFAIPI.....QTKSGGTRTGNVTLABGPPA 132 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 000.7 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext em_estba:..
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## gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Silbaq, F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
99003183
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bolotin, A., Ehrlich, S.D. and Sorokin, A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A.
                                                                                                                                                                                                                                                                                           /organism="Mycobacterium leprae"
/mol type="genomic DNA"
/db_kref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"
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A linear GSS 17-DEC-2002 aeruginosa genomic clone
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CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 16
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is htrA (95%)
Class: shotgum
High quality sequence start: 30
High quality sequence stop: 1408.
Location/Qualifiers
1. 1438
//organism="Lactcocccus lactis subsp. cremoris"
//mol_type="genomic DNA"
// strain="MG1363"
// db_tyref="learnoris"
// db_tyref="learnoris"
// clone lib="WG1363"
// clone
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317 ggrddagrogrrdrcractofrcaagcgggrcrtrcrdcracacagagrcraaaa
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Pseudomonadaceae, Pseudomonas.
1 (bases 1 to 959)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
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|||| GGTAAATCAGCCACACAATGTCAAAACTCTCTAAA 105
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Matches:
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pacel-60_1644.82 pacsl-60 Pseudomonas ac
pacel-60_1644, genomic survey sequence.
BZ549048
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Pseudomonas aeruginosa
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126.50
45.45%
30.30%
18.74%
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GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 126
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188
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120.50
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Best Local Similarity:
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CB679186.1 GI:29682911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TACGGCCTCGACAAGCCGTCCGGCGCGCGGTGGGGAAGACGGCCCGGCG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 GTCGCGCTGAACGTCGCCGACCAGTTGAAGAAAGCCGGC-----AAGGTCAGTCGC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProlleAsn 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 959
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Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Bedomonnes aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Fax: 206885744
Exa: 206885744
Email: craymond@u.washington.edu
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                                                                                                                                                               Class: shotgun.
Location/Qualifiers
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47.29%
31.01%
18.07%
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CB679186/c
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PORWARD: gra aaa cga cgg cca gtg

FORWARD: gga aac agc tat gac cat g

BACKWARD: gga aac agc tat gac cat g

Plate: 02 row; F column: 19

Seq primer: gga ac agc tat gac cat g.

1. 726

Anolitype="mRNA" sativa (japonica cultivar-group)"

Anolitype="mRNA" sativa (japonica cultivar-group)"

Anolitype="mRNA" sativa (japonica cultivar-group)"

Anolitype="mRNA" sativa (japonica cultivar-group)"

Anolitype="lag" sativa" sativa (japonica cultivar-group)"

Anolitype="lag" sativar-group "

Alab-host="lag" sativar-group"

Alab-host="lag" sativar-group"

Anolitype="lag" sativar-group"

Anolitype="lag" sativar-group "

Anolitype="lag" sativar-group "

Anolitype="lag" sativar-group group gro
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29 GlnIleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGly 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 ---ATCCGGCGAGCTCAGAAACCCTT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GlyThrArgThrGlyAsnValThrLeu 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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Saccharum officinarum
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/clone="bhost="bHi0B-T1" phage-resistant E. coli"
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/note="Websize acid-treated seedlings"
/note="Websize acid-treated seedlings grown
in hydroponic culture. After 12 days, medium was
supplemented with a solution of 1 mM ABA. Roots and leaves
were misted with a solution of 1 mM ABA. Roots and leaves
were misted after 3 % /, 12, and 24 hr and material from
all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
different Draili sites of the pMR188-FI3 vector (5-prime
Draili site is CACTGTGTG, 3-prime Draili site is
CACCATGTG). XhoI excises the cDNA insert."
                                                                                                                                                                                                                  Sufaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Engales; Poaceae; PACCAD clade; Panicodeae; Andropogoneae; Sorghum.

1 (bases 1 to 590)

2 Cordonnier-Pratt, M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D., Eastman, A. and Pratt, L.H.

5 Unpublished (2003)

6 Unpublished (2003)

7 Other_ESTS: ABA1_2_F06.gl_A012
Conteat: Cordonier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fex: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt Guga edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A. & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                         LBYLDBUZ 122 F06.bl A012 Abscisic acid-treated seedlings Sorghum bicolor CDNA clone ABAI_22_F06_A012 3', mRNA sequence.
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POLYA=Yes.
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Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AAAGTICGICGICGIGGCIIGAAIGIGGACTICGCICCGGAICCAAIIGCAIAI----- 119
                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Saccharum.
                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                               -----Thr 77
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Centro de Biología Molecular e Engenharia Genetica
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parridadounicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
through the Brazilian Clone Collection Center (BCCC) at
Plate: 058 row: G column: 06
Seq primer: T7 Promoter Frimer.
                                                                                                                                                         49 LeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAla
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Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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US-09-684-215B-4 (1-132) x AZ934428 (1-603)
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Solanum tuberosum
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43.44%
29.51%
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Best Local Similarity:
                                                                     Scores:
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                                                                                                                                           Query Match:
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BQ514888/c
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DEFINITION
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Pred. No.:
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DNB Ba0002108r B. japonicum BAC library Bradyrhizobium japonicum
Genomic, genomic survey sequence.
AZ934428
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Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bradyrhizobiaceae; Bradyrhizobium.
I (bases 1 to 603)
Townins, J. P., Wood, T. C., Stacey, M. G., Loh, J. T., Judd, A.,
Goicoechea, J. L., Stacey, G., Sadowsky, M. J. and Wing, R. A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                        ThralaMetalaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
                                                                                                                                                                       510
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                                                                                                                                             27
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                                                                                                                                                                                                     28 ------GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro
                                                                                                                                                                                                                                                                                                                      64 ValValGlySerAlaProAlaAlaSerLeuGlyIleSer------
                                                                                                                                             10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 126
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          807
38
20
47
47
            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Tel: Octabn Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Location/Qualifiers
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Class: BAC ends
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AUTHORS
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LOCUS
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BQ514888
EST622303 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIO81 3' end, mRNA sequence.
BQ514888.1 GI:21373757
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1 (Sabass 1 to 758)
Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)
Other ESTS: ESTS2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Bmall: potato-array@figr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
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/clone lib="B. japonicum BAC library"
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36
117
112
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Matches:
Conservative:
Mismatches:
Indels:
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FEATURES

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BEZ561390 1033 bp DNA linear GSS 17-DEC-2002 pacs2-164_3239.y3 pacs2-164 Pseudomonas aeruginosa genomic clone
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E. Transcriptome analysis of the acoelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 TTCATACAGTTAGCACTAAAAGCATCCTCAAATACTCGGAGCTCTTCCCCAATATCGTCA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 GCATCTCGCGGTGGACAACATTTTGTAGAGTTGAATGGTGTTCTGATTCATGCTGTATA
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                                                                                                                                               Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao
Brasil
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Matches:
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                                                                           mansoni
Nat. Genet. 35 (2), 148-157 (2003)
22879926
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                                                                                                                                                                                                                                                                         Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@ig.usp.br
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Schistosoma mansoni
Bukaryota, Metazoa Platyhelminthes; Trematoda; Digenea;
Bukaryota, Metazoa Platyhelminthes; Trematoda; Schistosoma.

(bases 1 to 982)
Verigeidida, Schistosomatoidea; Schistosoma.

(bases 1 to 982)
Verigovaki-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Verigvaki-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Kitajima, V.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leitte, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA linear EST 14-SEP-2003
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532 TIGATCCAATCIGGAAAAGTTCTTCGTGCTGGTTTGAATATTGAAATCGCTCCAGACCTG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 ACATCAGCAGGTGTTGGATTTGCAATCCCTTCTTCAACTGTGTTGAGAGTTGTGCCCCAG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 -----ATTGCCAACCAACTTAATGTTCGAAATGGAGCACTGGTTTTGCTGGTACCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlySerAlaProAlaAlaSerLeuGly-----74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGln 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 IleArgSerGlyGly-----GlySerProThrValHisIleGlyProThrAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 PheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 IleSerThrGlyAspVallleThrAlaValAspGlyAlaProIleAsnSerAlaThrAla 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetalaAspAlaLeuAsnGlyHisHisPiroGlyAspValIle 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TIGTATAAAGCCCTGGATAACTATAACATAGGTGAAGTT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                /mol_type="mRNA"

/collivar="Kennebec or Binjte"

/db xref="taxon:4113"

/clone="STMIO81"
                                                                              organism="Solanum tuberosum"
                                                                                                                                                                                                   tissue_type="mixed tissues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC80132
MA3-9999U-M294-C03-U.B MA3-0001 Schi
MA3-9999U-M294-C03.B, mRNA sequence.
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                               location/Qualifiers
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CD080132.1 GI:34631128
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.554
113.00
42.98%
29.82%
16.74%
       Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.: Alignment

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534

40

S

654

85

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS DEFINITION

RESULT 9 CD080132

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Percent Similarity:
Best Local Similarity:
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VERSION
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AUTHORS
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MEDLINE
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COMMENT
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AZ933900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AGGGTGGCCTGCAGGTGGGCGATGTGATCCTCAGCCTGAACGGCCAGTCCATCAACGAGT 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValValGlySerAlaProAlaAlaS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 erLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerAspAsnPheGlnLeuSerGlnGlyGlyGln-----GlyPheAlaileProileGly 21
                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 1033)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .1033
/organism="Pseudomonas aeruginosa"
/organism="Pseudomonas aeruginosa"
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/strain="2-164"
/db xref="taxon:287"
/clone="pacs2-164"
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/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 IGATICGCAACGGCCAGCGCAAGTCCCTGAGCAIGGCGGTAGGCAGCCTT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnAlaMetAlaIle-AlaGlyGlnIleArg----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033
41
20
56
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
  pacs2-164_3239, genomic survey sequence
                                                                                                                                                                                                     Genome Center
University of Mashington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Exar: 2066857244
Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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                BZ561390 T
BZ561390.1 GI:27181349
                                                       Pseudomonas aeruginosa
                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.78
106.50
44.20%
29.71%
15.78%
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Best Local Similarity:
Query Match:
DB:
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           ACCESSION
VERSION
KEYWORDS
SOURCE
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719 bp DNA linear GSS 24-APR-2001
BJ BA0001B03r B. japonicum BAC library Bradyrhizobium japonicum
AE933900
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                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.

(bases to 719)
Towkins, J. P., Wood, T. C., Stacey, M. G., Loh, J. T., Judd, A.,
Goicoechea, J. L., Stacey, G., Sadowsky, M. J. and Wing, R. A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| |||||||||||| :::
44 GGCATCGGCTTTGCGATCCTTGTCAACATGGAGCGCGTGGTCGTCGCTTCCGCCAAGGGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGGTTCCGCGCAATCGACGGCAGCAGCGGCGAAGCCGCTCAAG---CTCGCGATC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGGCCAGACCGTGGATGCATTGCCTTCGACTACCGCTTCGCGACGCGTCCACTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 GlyGlnGlyPheAlaileProlleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GlySerProThrValHisIleGlyProThr
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/db_xref="taxon:375"
/lab host="Ex col!"
/clone llb="B. japonicum BAC library"
/note="Vector: pindigo536; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Urodan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                Genome Res. 11 (8), 1434-1440 (2001)
21376150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 671.
Location/Qualifiers
1. .719
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                                                                                                                                                         Bradyrhizobium japonicum
Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Class: BAC ends
                                                                                                                AZ933900.1 GI:13775960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.42
103.50
37.86%
24.29%
15.33%
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pacsi-60 1644.sl pacsi-60 Pseudomonas aeruginosa genomic clone pacsi-60 1644, genomic survey sequence. BZ549047. GI:27152628 GSS. 205 111 ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeuAlaGluGlyPro 130 395 GCGCTGGAGACCCCGACGCCGCCAACGAGCTCGTCATCACTGCGCTTCGCCG 454 33 GlyGlyGlySerProThrValHislleGlyProThrAlaPheLeuGlyLeuGlyValVal 52 73 LeuGlylleSerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAla 92 32 53 AspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSer 72 4 SerAspAsnPheGlnLeuSerGlnGly-----GlyGlnGlyPheAlalleProlleGly 21 GGTGGCCTGCAGGTGGGCGATGTGATCAACAGCCTGAAACGGCCAGTCGATCAACGAGTCC 254 GGCGT-GGTGATCCAGGAAGTGAACAACGATCTCGCCGAGTCTTCGGCCTC-----ThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAsp 106 944 748 748 748 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 22 GlnAlaMetAlaIleAlaGlyGlnIleArgSer--US-09-684-215B-4 (1-132) x BZ549047 (1-947) 6.57 103.50 44.74\$ 32.46\$ 15.33\$ Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 12 BZ549047/c LOCUS DEFINITION REFERENCE AUTHORS JOURNAL COMMENT FEATURES TITLE ORIGIN g ò g d  $\delta$ 유 ò ò  $\delta$ 

TOTAL PARK

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Location/Qualifiers

1. 726

/organism="Photorhabdus luminescens"
/organism="Photorhabdus luminescens"
/mol_type=""enomic DNA"
/etrain="W14"
/db_ref="texon:29488"
/clone="Primary phase variant"
/clone="primary phase variant"
/clone lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                    GSS 14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                  Photorhabdus luminescens
Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 726)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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179 TCATTCGATAAAAGTGAAAATGGTGAAACGCCAGAAGGGTTGGGGTTCGCTATTCCGACT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: ffrench-Constant RH
Contract: farench-Constant RH
University of Bath
South Building, Bath BA2 7AY, UK
South Building, Bath BA2 7AY, UK
Far: (44) 1225 826621
Fax: (44) 1225 82679
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For
This is one of 2,122 random cands from the M13 library. For the M13 library of the M13 library of
                                                                                                                                                                    AQ989479 14-AUG-2
Rfc00025 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00025, genomic survey
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726
139
111
111
2
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Matches:
Conservative:
Mismatches:
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Gaps:
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Class: shotgun.
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103.00
46.55$
33.62$
15.26$
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58GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlylle 75	N AJ558965 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 1 09 a08, mRNA sequence. AJ558965	Antirinhum.  1 (bases 1 to 765)  Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z. Antirinhum EST collection Unpublished (2003) Contact: Schwarz-Sommer Z Molekulare Pflanzengenetik MPI fuer Zuechtungsforsednung Carl-von-Linne Weg 10, D-5029, Germany.  Location/Qualifiers  1 765    1 765     1 765     1 765     2 400   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161   1 161	/clone_lib="Antirrhinum majus whole plant" ent Scores: 6.79	-684-215B-4 (1-132) x AJ558965 (1-765)  10 SerGinGlyGlyGlnGlyPhealaileProlleGlyGlnAlaMetAlaileAlaGlyGln 29  11 ACCTCGGCGGTGTAGGATTTGCGATCCTTCATCGACAGTAAAGATAGTGCTCAG 370  12 ACCTCGGCGGTGTAGGATTTGCGATCCTTCATCGACAGTAAAGATAGTGCTCAG 370  13 IleArgSerGlyGlySerProThrValHisleGlyProThrAlaPheLeuGlyLeu 49  13 IleArgSerGlyGlyGlySerProThrValHisleGlyProThrAlaPheLeuGlyLeu 49  15 Ill
Oy Db Oy Oy Db ANSSULT 14 ANSS8965	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE TOURNAL COMMENT FEATURES	Alignment S. Pred. No.: Score: Percent Sim Best Local, Query Match	60-sn

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| 1.859 | forgatism="Datio rerio" | forgatism="Datio rerio" | forgatism="Datio rerio" | forgatism="Datio rerio" | forgatism="Datio (1955" | forgatism="India (1978) | forgatism="Capa Emb2" | forgatism="MoI Capa Emb2" | forgatis
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Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Meopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

El (Masses it os 859)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Bioscience Corporation

Clone distribution: MGC Glone distribution information can be found through the I.M.A.G.E. Consortium/Linn at:

http://image.llh.gov

Plate: LiAM14289 row: k column: 14

High quality sequence etop: 662.
                                                                                                                                                                                                    CA480614
AGENCOURT 10739220 NCI_CGAP_ZEmb2 Danio rerio cDNA clone
IMAGE:6789351 5', mRNA sequence.
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584 GTCAGGAGTAGGGCCGAGCTATACAAAACACTGGATGAGTATTCCATCGGAGACAAAGTG 643
89 IleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIle 108
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204 TAAGCTTCGGGGGCCTCACCTTCCAGGCGTTCTGGA-----ACAGGCTCCTCCTTGGTC 257
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                                                                                                                                                                                                                                                                                                                                                     24 MetalallealaGlyGlnIleArgSerGlyGlyGlyGlySerProThr---ValHislleGly 42
                                                                                             99 TCAGGGGCATTTGGGCAGATGCGCTTGAGTGGGGGGGACACCCTCCAAGTCCTTTGTGTGCA
                                                                                                                                        43 ProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGln
               7 PheGlnLeuSerGln-----GlyGlyGlnGlyPheAlaIleProIleGlyGlnAla
                                                                                                                                                            63 ArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThr
                                                                                                                                                                                                                                                                                      119 ThrArgThrGly 122
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Bonaldo, Ph.D.

CIONA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage.html

Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                 A1597611 423 bp mRNA linear EST 21-APR-1999 tnlsf02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167707 3' similar to TR:\[\tilde{O}08664 BCL7C MRNA. i, mRNA sequence.\]
A1597611. GI:4606659
                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarthini, Hominidae, Homo.

(Lôasea 1 to 423)

NCI/MINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/MINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

(Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tisgue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                   LeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGly 118
                                                                                                              ::::::|||||||
572 GTAGATGGGCACAGTGTGGGTGACACCATCACCAGAGTCCATCACGATACCAGTGGTACG 513
592 CCTCTCAGCTGTGGTGGTGAAGCTGTAGCCTCTCTCGGTCAGGATCTTCATGAGGTAGTC 633
                              ThralayalAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAla----- 98
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Indels:
Gaps:
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Contact: Stephen 1. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Arrayed by:
Matchaw Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarbatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                           Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Washu Zebrafish Est Project 1998

L Unpublished (1998)
BI350520 transportation adult brain Danio rerio cDNA clone IMAGE:4955073 5' similar to SW:ACT2_FUGRU P53485 ACTIN, CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.rzpd.de)
Seq primer: T7
High quality sequence stop: 301.
Location/Qualiflers
1. .499
                                                                                                                     2;, mRNA sequence.
BI350520
BI350520.1 GI:15044966
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(1-423)

US-09-684-215B-4 (1-132) x AIS97611

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us-09-684-215b-4.rst
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CA473840
AGENCOURT_10740457 NCI_CGAP_ZKid1 Danio rerio cDNA clone
IMAGE:6794807 5', mRNA sequence.
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319 CTCCTGCTCAAAGTCAAGGGCCACATAGCAGAGCTTCTCCTTGATGTCACGGACAAT--- 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AlaAspAla-----LeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cypriniformes, Cyprinidae, Danio.

1 (bases 1 to 870)
1 (bases 1 to 870)
1 (harbac/hmgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 SerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMet 95
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                                                    /dev stage="adult"
/lab_host="B. coli DH10B"
/lab_host="B. coli DH10B"
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/note="Vector: pZIPLOX; Site 1: Not1; Site 2: Sal1;
/note="Vector: pZIPLOX; Mass constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GlyGlnGlyPheAlalleProlle
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                          499
117
117
117
6
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Matches:
Conservative:
Mismatches:
Indels:
/clone="IMAGE:4955073"
/sex="mixed male and female"
/tissue_type="brain"
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CA148171
SCEZRZ1017F10.g RZ1 Saccharum officinarum cDNA clone SCEZRZ1017F10
S.', mRNA sequence.
CA148171.1 GI:35048941
EST.
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM14303 row: n column: 22
High quality sequence stop: 671.
Location/Qualifiers
i. 870
//organism="Danio rerio"
//mol Lype="mRANA"
// Ab xref="Laxon:9955"
// Clone line "MAGE:6794807"
// Ab host="MAGE:6794807"
// Ab host="MAGE:6704807"
// Ab host="
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Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Pantocideae, Andropogoneae, Saccharum.
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BI721127.1 GI:15696822

VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL	FEATURES		ORIGIN	ORIGIN	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	US-09-684-	Å å	g & 2	3 & E	ìò	qq	ò
AL AL	COMMENT Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Universidade Estadual de Campinas SP, Brazil Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137	Email: parrudeaun.camp.or Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 017 row: F collumn: 10 Seq primer: T7 Promoter Primer. FEATURES	e O	/crote="Torgan: Shoot-root transition zone from young plants (large insert library); Vector: pSportl; Site_1: Sall; Site_2: Nor!, An unidirectional CDNA library generated from [Shoot-root transition zone from young plants (large insert library)]. cDNA was prepared from polyA+ mENA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"	Alignment Scores: 9.61 Length: 444  Pred. No.: 97.00 Matches: 26  Percent Similarity: 47.62\$ Conservative: 14  Best Local Similarity: 30.95\$ Mismatches: 26  Query Match: 14.37\$ Gaps: 2	US-09-684-215B-4 (1-132) x CA148171 (1-444)	54 ASIASIGIYASIGIYALAARGVAIGIDARGVAIVAIGIYSERALAProAlaAlaSerLeu 7	Db 92 ddccrrdcrccgaccggcaggggrrrcgcrggraacarrgrrcrrdcrcarcarcgrr 151	Qy 83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102	Qy 103 HisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 122 Db 212 GGCGTCGGGGATCAGGTGACCTTGACAATCCGGCGAGGC 250	Qy 123 AsnValThrLeu 126 :::        Db 251 TCTGAAACCTC 262	RESULT 20 RI731127	LOCUS BI721127 543 bp mRNA linear EST 19-SEP-2001 DEFINITION 1031054B10.yl C. reinhardtii CC-1690, Stress II (normalized),	Lambda Zap II Chlamydomonas reinhardtii cDNA, mkNA sequence. ACCESSION BI721127

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chlamydomonas reinhardtii

Chlamydomonas reinhardtii

Chlamydomonas reinhardtii

Enkaryota, Viridiphantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadacaee; Chlamydomonas.

Chlamydomonadacaee; Chlamydomonas.

CE 1 (5043)

RS Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,

R Grossman, A., Chang, C.-W., Davies, J., Silflow, C. and Stern, D.,

Analyses of the Chlamydomonas reinhardtii Genome: A Model,

Unicellular System for Analyzing Gene Function and Regulation in

Vascular Plants. Project: 1031

Anchants. Project: 1031

Contact: Charles Hauser

Contact: Charles 
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Sorghum bicolor (sorghum)

Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

Bases 1 to 551)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.

An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Soriences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 543 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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1. .551

1. .551

2. organism="Sorghum bicolor"

Aportarism="Sorghum bicolor"

Aboxref="taxon:4559"

Aboxref="taxon:4559"

Actione lib="Light Grown [LG1]"

Anote="Organ: 10 to 14-day-old light-grown (greenhouse)

seedlings; Vector: Lambda Zap; Site 1: Xho1; Site 2:

seedlings; Vector: Lambda Zap; Site 1: Xho1; Site 2:

sector lambda ZaP II. Clones to be sequenced were

prepared by mass excision."
                                                                                                                                                                                       AW285527

LG1_241_G05.g1_A002_Light_Grown 1 (LG1) Sorghum bicolor cDNA, mRNA sequence.

AW285527.1 G1:6675371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerbeu
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High quality sequence start: 16
High quality sequence stop: 552
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                         236 GGCGTCGGAGATCAGGTGACCTTGACA---
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LG1_241_E05.g1_A002_Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
That Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
Fax: 706 583 0210
Smail: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below bred quality 16. The threshold for highest quality sequence
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| GGICTIGCTCCAACCGGCAGGGTTTIGCTGGTAATATIGTTCTGGGTGATATCATCGTT 175
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Sorghum bicolor
Sorghum bicolor
Sukaryota, Virighlantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Virighlantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.

1 (bases 1 to 546)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
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    378 GGCTCCCTGGTGCTGGGGCGACATCATCACAGGCATTGACGGCAAGGCCGTAAAGAACTAT 437
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High quality sequence stop: 546
POLYA-Yes.
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103 H18FroGyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGly 122	123 AsnValThrLeu 126 :::        280 TCAGAAACCCTT 291	RESULT 23   BUS57763	Homo Eukan Mamme Marin Natio Unpul Contic Tissi CDN CDN CDN CDN CDN CDN CDN CON CDN	http://image.llnl.gov Plate: LLCM2798 row: f column: 07 L. 1093 I. 1093 / crganism="Homo sapiens" / mol_type="mRNA" / db_xerf="texaon:9606" / clone="TwAGE:6885799" / tissue_type="adenocarcinoma, cell line" / lab host="Plat108 (phage-resistant)" / lab host="Plat108 (phage-resistant)" / clone lib="NNIH MGC 107" / note="Grgan: breast; Vector: pOTB7; Site_1: EcoR1; / note="Grgan: breast; Vector: pOTB7; Site_1: EcoR1; / site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sitess using the following 3 adaptor: GGCAGGAGGG. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University ing Hong in the laboratory of Gerald M. Rubin (University ing Ralefornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).	ORIGIN  Alignment Scores: Pred. No.: 96.00  Percent Similarity: 35.43%  Ober Local Similarity: 27.43%  Mismatches: 14.28  Mismatches: 46  Mismatches: 46  Mismatches: 68  Description of the property of the p	US-09-684-215B-4 (1-132) x BU557763 (1-1093)  Qy 23 AlaMetalaileAlaGlyGlnIleArgSerGlyGlyGlySer 36  Dh 789 GrycocofGrangGargCaracabaAnGGGGGGGTGAAGGGGGTGAAGGGTAA 730

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1394 bp DNA linear GSS 17-DEC-2002
Pseudomonas aeruginosa genomic clone msh2_4761,
squence.
                                                                                                                                                                                                                                                                                                         ----PheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAla 59
----PheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAla 59
----PheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAla 59
----PheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAla 59
----PheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAla 59
                                                                                                                                                                                                      AAACCAGTCCCGGTGGAGGATCTCTCGGGGAGGTAATTGGGTGC 553
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'R. and Olsen,M.V.
uence variation among multiple isolates of
1009 library
Olso, In press
Raymond
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|lib="msh"
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:le, WA 98105-2145, USA
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BX674871 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0037i.j.05 5prim, mRNA sequence.
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Fax: 33 (0) 5.61.28.53.08

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Clone distribution: AGENAB Resource centre. Francois PIUMI,

genome (LREG), Domaine de Vilvert, 78352, Jouy-n-Josas cedex,

FXANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.27.73

Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.
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Sus.
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                32 SerGlyGlyGlySerProThrVal---HislleGlyProThrAlaPheLeuGlyLeuGly
                                                                                                                                                                                                                                                                             GlyGlyGlnGlyPheAlalleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg
/clome_lib="WARC 4FIG"
/note="Vector: poDNA3.1, Site_1: EcoRI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 647)
Bonner,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S., Soares,M., Bonaldo,F. and Hatey,F. Tobrary Unpublished (2003)
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(Dases I to 600)

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages

Contact: Smith TPL
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       US-09-684-215B-4 (1-132) x BZ576076 (1-1394)
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Fax: #9 30 910 1212 1120
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above BST is generated is available at the
amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (http://www.rzpd.de)
PCR PRimers
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTG 3' (MI3RSP)
BACKWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGGTG 3' (MI3RSP)
Insert Length: 1200 Std Brror: 0.00
Seq primer: 5'-CCGGTCCGGAAAGGGGGGT-3' pSport3/86
High quality sequence stop: 677.
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/lab_host="E.coli, Xil blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name
/note="Vector: pSporti; site 1: Sal1, KpnI, BcoRI (5');
Site_2: NotI, BamHI, HindIII (3'); OligodT primed and
directionally cloned in pSporti vector using a NotI
(5'-pGACTAGTICTAGATGCGAGGGGCGCCC (T)15-3' and a SalI 5'-
TGGACCAGGGTCCG-3'adapters (Glbco BRL)."
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                                           laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.(3-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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/db_xref="taxon:7739"
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                                                                                         /mol_type="maxa."

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/clone="scaco037i.j.0s"

/clone="yope="mixad"

/clone=Tib="Sus Scrofa library (scac)"

/clone=Tip="sus Scrofa library (scac)"

/clone=Tip="sus Scrofa library (scac)"

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/noce="yope="mixad"

/noceptal intestine,

uterus, adranals, bulbo uretral gland, cerebral trunk,

epididymis, female gonad, gall-bladder, hippocampus,

large intestine, male gonad, melanocytes, stomach, udder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 AGCAATTCTGGA-----ACAGGCTCCTCGTTGGTCAGCATCGGGGGTTCATCCGTGCCG 382
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Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647
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                                                                         organism="Sus scrofa"
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mRNA sequence.
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Lauraryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rutinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

(Spriniformes; Caparion; Caparion; Mammalian Gene Collection (MGC)

(Mucholished (1999)

(Contact: Robert Strausberg, Ph.D.

(Contact: Robert Strausberg, Ph.D.D.

(Contact: Robert Strausberg, Ph.D.D.

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/mol type="mmm" refiled
/mol type="mmm" refiled
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/clone="mmods:6805289"
/lab host="DHJ0B (T1-resistant)"
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/note="Organ: kidney; Vector: pCMV-SPORT6.1; Site_1:
/note="Organ: kidney: note: pcm, refiled by J.
/mang (Research Genetics, Invitrogen Corp) from tissue
/donated by L. Son (Harvard University). Note: this is a
/note: pcm, refiled by Library."
                                                                                                                                                                                                                                                                                                         CAY/5497 1067943 NCI_CGAP_ZKid1 Danio rerio cDNA clone IMAGE:6905289 5', mRNA sequence.
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                          GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
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                                                                                                                                                      125 ThrLeuAlaGluGlyProPro 131
                                                                                                                                                                                                             839 CACGICNGGGCCALTCCGCCT 859
                                                                                                                                                                                                                                                                                                                                                                                                                       CA975497
CA975497.1 GI:27508151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.5
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                                                                                                                                                                                                                                                                                                         CA975497/c
                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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AUTHORS
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COMMENT
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                                                                                                                                                                                                       셤
             Triticum aestivum (bread wheat)

ISM Triticum aestivum

ENKaryota, Varidiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Boideae; Triticeae; Triticum.

CE (base I to 881)

RS Allard, F., Grosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F., Mizak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F. Mizak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F. Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, P. Mizak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, Functional Genomics of Abiotic Stress In Wheat and Canola Crops Contact: Wm L Crosby

Bioinformatics

Bioinformatics

Contact: Wm L Crosby

Bioinformatics

Contact: Wm L Crosby

Bioinformatics

Contact: Wm L Crosby

Bioinformatics

Contact: Wm Saskatchewan, Department of Computer Science

11.69 56 2033

Email: fgas_ests@cs.usask.ca

This sequence: is the direct result of the Base calling software Lucy

(default parameters) has been run on this sequence. Lucy identified the region [123,622].

Plate: Talt547 row: K column: 14.

Plate: Talt547 row: K column: 14.

Localion/Qualifiers

Localion/Qualifiers
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db_type="mRNA"
/db_type="taxon:4165"
/db_type="taxon:4165"
/lab_host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS: Talt5"
/note="organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype P1178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 GECTICALIGACICGGGITIGGGCICIGGCITIGGITCIGGITIGGGCALCGGCICANGC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 TICGGTICGGGTITIGGCATCGGCTCAGGCTTGGGCTCTGCGTTGATC---CACTGGCC 796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheGlnLeuSerGlnGly---GlyGlnGlyPheAlaileProlleGlyGlnAlaMetAla 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ilealaGlyGlnIleargSerGlyGlyGlySerPro---ThrValHisIleGlyProThr
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                                                          ORGANISM
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Oy 44 ThrAlaPheLeuGlyLeuGlyValValAs bb 462 ATTGCGTATCAGCTTAACGTCGGTGA Oy 64 ValValGlySerAlaProAlaAlaSerLe 117 GTTCCCCGGGGGGACGCTGGAAAAGC Oy 75leSerThrGlyAspVallleTh Db 357 GGCAATATTGTCCTGGGGGACGTCATTGT Oy 93 ThrAlaMetAlaAspAlaLeuAsnGlyHi 1	*	·	
Db 688 CTCAAAGTCAAAGGCACATAACAAAGTTCCTCTTGATGTAACGGACAAT	TITLE Expressed genes in Triticum aestivum JOURNAL. Unpublished (2002)  CONTACT: Tadasu Shin-1  Contact: Tadasu Shin-1  Contact: Tadasu Shin-1  Contact: Todentic Resource Information National Institute of Genetics 1111 Yata, Mishina, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81	Alignment Scores: 34.6 Length: 728  Score: 94.50 Matches: 37  Score: 20  Best Local Similarity: 27.41% Mismatches: 53  Query Match: 14.00% Indels: 5  DB: 12 Gaps: 5  US-09-684-215B-4 (1-132) x BJ285991 (1-728)	10 SerGlnGlyGlyGlnGlyPheAla 10 SerGlnGlyGlyGlnGlyFl

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GCAGGICTAGTICCTACAGGCAGGGGTTTTGCC 358
Leugly---- 74
                                                                                     GlyAsnValThrLeuAla 127
:::
ATTCCGATAGCCCTGTCG 202
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Aas03793 M. Tuberc
Aa140768 Nucleotid
Aa140788 Nucleotid
Aa14078 Nucleotid
Aa26353 Mycobacte
Aa28343 Mycobacte
Aa220194 Mycobacte
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1. 396
4.tag=
7coduct= "Ral2 protein"
/note= "No start or stop codon"
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ADA26363
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AAI99683_01
AAI9466
AAV44342
AAX1900
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AAX191114
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    AAL40769;
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Aa120206 Mycobacte
Aa140770 Nucleotid
AbX14140 DNA encod
Aa447078 Mycobacte
Aa447077 Mycobacte
Aa428336 Mycobacte
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1493.479 Million cell updates/sec
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                                                                                                                                                                                                                                                   US-09-684-215B-4
675
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
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                                                                                                                                                            April 29, 2004, 20:30:12; Search time 375.474 Seconds
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                            OM protein - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3373863 segs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAL40772
AAZ20206
AAL40770
ABK14140
AAD47078
AAD47077
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
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Database

Minimum DB seq Maximum DB seq

Scoring table: Perfect score:

Sequence:

Run on:

Score

675 675 675 675 675 675

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Kba C-terminal fragament of serine protease antiquen WTB13A of for the recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting seriam antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
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Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encades fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure, Fig 5, 39pp, English

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Mammalia. Unidentified. Chimeric.

Key

Location/Qualifiers
4. .666
//teg= //teg= //teg= "Ral2-mammaglobin fusion protein"

99US-0158585P.

07-OCT-1999;

Skeiky Y, Guderian J; WPI; 2001-266299/27. P-PSDB; AA022141.

(CORI-) CORIXA CORP

06-OCT-2000; 2000WO-US027652.

WO200125401-A2

12-APR-2001

Nucleotide sequence encoding Ral2-mammaglobin fusion protein.

(revised)
(first entry)

06-AUG-2003 03-OCT-2002

Guderian J;

Skeiky Y,

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 can polypeptide, comprising a polynucleotide sequence of Ral2, a 14 molecular fragment of Series proteide sequence of Ral2, a 14 molecular function and a neterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing steadhe and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ral-mammaglobin fusion protein. (Updated on 06-AUG-2003 to correct OS field.)
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AAL40772 standard; DNA; 672

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                                                                                                                                                                                                                                                                                                                           IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
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98US-00223040.
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P-PSDB; AAY32071.
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30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                           101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                             41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                  25 ACGGCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCTGGGATCGCCATTCCCGATC
                                                                                                                                                                                                                                            61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyA8pVal
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C, 225 G, 121 T, 0 U, 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence encoding Ral2-DPPD fusion protein.
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/*ttag= "Ral2-DPPD fusion protein"
/product= "Ral2-DPPD fusion protein"
                                                                                                                                                                                                                                                                                                                                                                  ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                               1.53e-54
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 Sequence 702 BP; 127 A; 229
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
Chimeric.
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                      Alignment Scores:
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                                                                        Query Match:
DB:
                                 Pred. No.:
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(revised)
(first entry)

29-AUG-2003 08-MAY-2002

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14 bac-terminal fragment of serine protease antigen MTB32A of MD C-terminal fragment of serine protease antigen MTB32A of MD C-terminal fragment of serine protease antigen MTB32A of production the confidence of the sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cutaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis and an indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence conception to indicate the DNA encoding the Ral2-DPPD fusion protein
                                                                                                                                                        Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                             Example 1; Fig 3; 39pp; English.
                                                                             WPI; 2001-266299/27.
P-PSDB; AAO22139.
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Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.53e-54 675.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 25 ACGGCCCGCGTCCCGATAACTTCCGAGCTGTCCCAGGGTGGCCAGGATTCGCCATTCCCGATC g ò

US-09-684-215B-4 (1-132) x AAL40770 (1-702)

20 84 g

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61 ValGlnargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 

264

80

81 IleThralaValaspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

g

ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 385

ABK14140 standard; DNA; 702

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/partial
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(pos:353. .355, aa:Xaa) /transl_except= (pos:970. .472, aa:Xaa)
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which alters the reading frame. Xaa= In frame stop codon" /partial
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/transl_except= (pos:450. .452, aa:Xaa) /transl_except=
/pos:621. .623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon" дв; Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24. antigenic fusion protein Ra12-DPPD (Mtb24) Location/Qualifiers
1. 702
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/product= "Mtb24 #1"
/partial /*tag= c /product= "Mtb24 #3" Mycobacterium tuberculosis DNA encoding Chimeric. Key CDS SGO 

US2002009459-A1

97US-00818112. 97US-00942578. 98US-00025197. 98US-00056556. 99US-00287849 01-OCT-1997; 18-FEB-1998; 07-APR-1998; 30-DEC-1998; 07-APR-1999; 24-JAN-2002 13-MAR-1997

SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A. (SKEI/) (DILL/) (ALDE/) (CAMP/) (REED/)

ď Campos-Neto Skeiky YA, Dillon DC, Alderson M, WPI; 2002-171134/22. P-PSDB; AAU74600, AAU76541, AAU76542. Reed SG,

New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.

for

Example, Fig 13; 62pp; English

The invention relates to a purified polypeptide which induces an immune

G; 121 T; 0 U; 0 Other; Sequence 702 BP; 127 A; 229 C; 225

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Guderian

Skeiky Y, Brannon M,

(CORI-) CORIXA CORP

WPI; 2002-759844/82. P-PSDB; AAE29703.

13-MAR-2002; 2002WO-US008223 13-MAR-2001; 2001US-0275837P

19-SEP-2002

ores: 1.53e-54 Length: 702 675.00 Matches: 132 675.00 Conservative: 0 Imilarity: 100.00% Mismatches: 0 6 Gaps: 0	5B-4 (1-132) x ABX14140 (1-702)	ThralaalaserAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlalleProIle 20	5 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84	GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	S GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGG	1 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 204	1 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80	S GTCCAACGCGGGGGGGGGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 264	1 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	5 ATCACCGCGGTCGACGCGCTCCGATCACTCGGCCACGCGATGGCGGACGCGCTTAAC 324	1 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120	5 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCT 384
nment Scores: No.: no.: nt Similarity: Local Similarity Match:	-215B-4	1 Thra	25 ACGG	21 GlyG	85 GGG	41 IleG	145 ATCG	61 Valg	205 GTCC	81 IleT	265 ATCA	101 GlyH	325 GGGC
Alignment Scores Pred. Score: Score: Percent Similari Best Local Simil. Query Match: DB:	US-09-684	ò	qq	ζ	Op.	ζŏ	Op	ζ	qq	ò	QC	ò	Db

Vaccine, immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; gene; antigen; ds. Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGCC BP AAD47078 standard; DNA; 1002 (first entry) 27-JAN-2003 385 AAD47078 RESULT

/*tag= a /product= "Ra35FLMutSA mutant antigenic protein" Location/Qualifiers 4. .996

Mycobacterium tuberculosis.

Synthetic.

120

957

ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

121

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleocide sequence encoding an antigen or an antigent fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculesis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for ralsing antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis RajsFLMutSA mutant antigenic protein encoding DNA 100 717 777 837 897 New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis. 40 9 80 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn GlyGlnalaMetalallealaGlyGlnIleArgSerGlyGlyGerProThrValHis ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other; 1002 132 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Disclosure, Page 80-81; 155pp; English. US-09-684-215B-4 (1-132) x AAD47078 (1-1002) 2.29e-54 675.00 100.00% 100.00% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
ES Alignment Scores: Pred. No.: 21 41 718 61 778 8 6 8 6 ö 셤 à g 8 g

ThrGlyAsnValThrLeuAlaGluGlyProProAla

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100 897 120 957

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us-09-684-215b-4.rng

AAD47077;

RESULT

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Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                          ValGInArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                             IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                                                                                                                                                                                                                      GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                  41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aa:Asp)
aa:Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein; antigen; serological sensitivity; tuberculosis; infection; vaccine; MTB32A; Ra32FL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
4. .96
/*tag= a
/*tag= a
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/transl_except= (pos:547. .549, as
/transl_except= (pos:550. .552, as
                                                                                                                                                                                                                                                                                                                                                                                                                           ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD28336 standard; cDNA; 1002
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01-FEB-2001; 2001US-0265737P.
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P-PSDB; AAE17566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                           Vaccine, immunity; diagnostic agent; gene therapy; Ra35 antigen; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
                                                                                                                                                                                        Mycobacterium tuberculosis mature Ra35 antigen encoding DNA
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
4. .996
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132
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGGC 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 79; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guderian J;
                                                                                       ВР
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675.00
100.00%
100.00%
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                                                                                       AAD47077 standard; DNA; 1002
                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-759844/82.
P-PSDB; AAE29702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                          27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2002
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the present invention relates to fusion proteins containing at least two

US-09-684-215B-4 (1-132) x AAD47077 (1-1002)

us-09-684-215b-4.rng

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compositions apprising such fusion proteins. The present invention particularly relates to mucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sex from individuals infected with increase treatment of tuberculosis infection. Sequences of the invention and useful for the tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and polynucleotides are useful as diagnosic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antifection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M, tuberculosis antibodies in a non-human proteins of the invention are also used as vaccines. WIB32A fusion proteins of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a CDNA encoding
Mycobacterium species antigens, nucleotides encoding them and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium species MTB32A (Ra32FL) mature protein
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1002 132 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-684-215B-4 (1-132) x AAD28336 (1-1002) 2.29e-54 675.00 100.00% 100.00% Secret Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;

GTCCAACGCGTGGTCGGGGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 837 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 957 717 Arcegeceracecerrececrregererrereacaacaacaacaacaaceacececacea 777 9 80 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlaglyPheAlalleProlle 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCTCT ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993 778 101 121 21 658 718 19 81 838 898 g g ć g ठे g ò 음 οp 8 8 õ ò  $\delta$ 

AAD28337 standard; cDNA; 1002 (first entry) AAD28337, AAD28337
IID AAD2
XX
AC AAD2
XX
XX
XX
DT 22-P
XX
XX
XX
XX
XX
XX
XX
XX
KW FUSI RESULT

Mycobacterium species Ra35FLMutSA mutant cDNA.

Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; RallFLMutSA; mutant; mutein; ss.

/*tag= a /product= "Ra35FLMutSA protein" Location/Qualifiers 

Mycobacterium sp.

WO200198460-A2

27-DEC-2001.

20-JUN-2001; 2001WO-US019959

20-JUN-2000; 2000US-00597796. 01-FEB-2001; 2001US-0265737P.

(CORI-) CORIXA CORP.

Skeiky Y, Reed S, Alderson M

WPI; 2002-147798/19. P-PSDB; AAE17567 Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.

Claim 67; Page 96-97; 136pp; English.

Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion protesins. The present invention particularly relates to nucleic acids encoding them and particularly relates to nucleic acids encoding fusion protesins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, custoful for eliciting an immune response in a mammal, e.g., human, consevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium in ediagnosis, treatment and prevention of Mycobacterium in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human continuation are also used as vaccines. WTB32A fusion proteins of the invention are also used as vaccines. WTB32A fusion proteins of the invention are useful as in vivo diagnostic agents Mycobacterium species Ra32FL mature protein mutant, Ra32FLMutSA

Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other;

1002 132 0 0 0 Length: Matches: Conservative: Mismatches: IndelB: 2.29e-54 675.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-09-684-215B-4 (1-132) x AAD28337 (1-1002)

657 40 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 598 Aceccecercearaacirceaeciereceaeceeecaeecaecearireecarirceare 21 GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 셤 ઠે

60 41 11eGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg

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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                                                                                                                                                 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                          730 GGGCAGGCGATGGCGATCGCGGGGCCAGATCCGATCGGGTGGGGGGTCACCACCGTTCAT 789
                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for
                                                                                                                                                                                        41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                       850 GICCAACGCGIGGICGGGAGCGCICCGGCGAAGICTCGGCATCICCACCACGAGGTG
                                                                                                                                                                                                                                                                                                                                                                          910 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                   ThralaalaaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProlle
                                                                                                                                                                                                                                                                      ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein, Mycobacterium, primer, PCR, amplification, probe, hybridisation, detection, vaccine, immunisation, infection, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1030 ACAGGGARCGTGACATTGGCCGAGGGACCCCCGGCC 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species nucleic acid sequence 50F
US-09-684-215B-4 (1-132) x AAX34251 (1-1068)
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97FR-00011325.
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P-PSDB; AAY04830.
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11-SEP-1997;
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                                                                                                                                                                                            GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                    957
                                                                                                                 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                         897
118 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGCCCACGA 777
                                                                         837
                                       80
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                                                                                                                                      ATCACGGGGTCGACGGCGCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGCGTTAAC
                                                                             Grechadecerecreseasecerecesedechademereceseareres
                                                                                                                                                                                                                                  GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCACGCGT
                                       ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim E, Pelicic V, Guigueno A; Y_i
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

2.46e-54 675.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

Claim 22; Fig 50D; 309pp; French.

696

909

849

80

ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 958 ACAGGGAACGIGACATIGCCCGAGGGACCCCCGGCC 993

Mycobacterium species nucleic acid sequence 50D.

Mycobacterium sp.

WO9909186-A2

(first entry)

06-JUL-1999

AAX34251;

98WO-FR001813 97FR-00010404.

14-AUG-1998; 14-AUG-1997; 11-SEP-1997;

25-FEB-1999.

Gicquel B, Portnoie D, Goguet De La Salmoniere (INSP ) INST PASTEUR.

WPI; 1999-181045/15. P-PSDB; AAY05000.

AAX34251 standard; DNA; 1068 BP

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10-OCT-2000;
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07-0CT-1999;
                 misc_feature
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                                                                                                                                        ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGACAACGGCAACGGCAACGGCAACGAA 924
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                                                                                                                                                                  GlyGlnAlaMetAlaileAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                                                                                               41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                            ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                                ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. tuberculosis DNA encoding antigen HTCC#1 fusion protein #4.
                  G; 186 T; 0 U; 0 Other;
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/note= "Xaa= In frame STOP codon"
                                             TbRA12-HTCC#1; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease; His Tag; ds.
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/note= "Region derived from TbRAl2"
427. .444
immunisation against a bacterial or viral infection
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                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1. 1629
/*tag= a
/product= "TDRA12-HTCC#1"
                                                                                                              US-09-684-215B-4 (1-132) x AAX34252 (1-1143)
                   Sequence 1143 BP; 189 A; 373 C; 395
                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                            2.66e-54
675.00
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Query Match:
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                                     Alignment Scores
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes Mycobacterium tuberculosis fusion protein, TDRA12-HTCC#1 and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                              Lodes
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                                                                                                                                                                                                                                                                                                                                                                                            Dillon DC,
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/*tag= c
/note= "Region derived from Thrombin"
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/*tag= d
/note= "Region derived from HTCC#1"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 8; 168pp; English.
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Best Local Similarity: 1
Query Match:
D8:
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84

204

80

9

324

Unidentified

Chimeric

12-APR-2001

Skeiky Y,

03-OCT-2002

AAL40771;

385

RESULT

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GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
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                                                                                                                                                                                                                                                                                                             85 decradectatidectaticectations and second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant nucleic acid molecule encoding
                                                                                                                                                             25 Acceccecerccearaacriccaecrerccaecececececececececariccearriccearc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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US-09-684-215B-4 (1-132) x AAL40771 (1-1742)
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89. .1156
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P-PSDB; AA022137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
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tusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14

KDa C-terminal fragment of serine protease antigen MTB32A of

Mycobacteriuu tuberculosis, and a heterologous polynucleotide sequence.

The recombinant fusion nucleic acids and polypeptides are useful for

providing stable and high yield expression of fusion polypeptides of both

eukaryotic and prokaryotic origin and to encode a protein product for use
as an antigen for detecting serum antibodies. The presence of serum

antibodies to M. tuberculosis antigens in an individual indicates that

the individual is infected with it. The fusion polypeptides are useful as

sources of proteins for monitoring binding of serum antibodies to fusion

proteins and as an immunogen to induce and/or enhance immune responses.

The coding sequences can be ligated with a coding sequence of another

molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and

can be used in vivo as a DNA vaccine. This polymucleotide sequence

represents the DNA encoding the Mycobacterium tuberculosis MTB32A protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1871 BP; 317 A; 617 C; 605 G; 332 T; 0 U; 0 Other;
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB38 antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                            /*tag= a
/product= "MTB32-MTB39F fusion polypeptide'
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P-PSDB; ADA26354.
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                                                                                                                                                                                                                                                                                                                        202 GICCAACGCGTGGTCGCGAAGCGCTCCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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                                               ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                             22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TbH9-Ra35MutSA;
mutant; mutein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium species MTB72FMutSA fusion protein encoding DNA.
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1. .2190
/*tag= a
/product= "MTB72FMutSA fusion protein"
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/note= "TbH9FL DNA fragment"
1603. .2187
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/note= "Ra35 DNA fragment"
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/*tag= b
/note= "Ral2 DNA fragment"
424. .1596
            US-09-684-215B-4 (1-132) x AAD47084 (1-2190)
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01-FEB-2001; 2001US-0265737P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolymucleotide sequence encoding an antigen or an antigenic fragment from my mucleotide sequence encoding a mantigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TGA, Leff, MIS, and 6H polymucleotides of the invention are used in methods for eliciting immune response in manmals. They are useful as vaccines to eliciting immune response in manmals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a nimal minal minal fusion protein. This fusion protein comprises and tot assambles mutant protein and Ralz protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                         Vaccine, immunity, diagnostic agent, gene therapy, TbH9, antigen;
RalShutsA, Ral2, MTB72MutsA, chimeric, gene; ds.
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                                                                                                                                                                                                                     Mycobacterium sp. MTB72FMutSA fusion protein, encoding DNA.
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1. .2190
1. stags a /products "MTB72FMutSA fusion protein"
/products "MTB72FMutSA fusion protein"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
958 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993
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                                                                               AAD47084 standard; DNA; 2190
                                                                                                                                                                                                                                                                                                                            Mycobacterium sp.
Mycobacterium tuberculosis.
Chimeric.
                                                                                                                                                               (revised)
(first entry)
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P-PSDB; AAE29709.
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Pred, No.:
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19-SEP-2002.

120 381

201

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Reed S, Alderson M; Skeiky Y, 

WPI; 2002-147798/19. P-PSDB; AAE17573.

Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.

Claim 81; Page 108-109; 136pp; English.

The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for elliciting an immune response in a mammal, e.g., human, cuseful for elliciting an immune response in a mammal, e.g., human, in vitro and in vivo assays for detecting humoral artibodies or cell-mediated immunity against M. tuberculosis, for the immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human and for raising anti-M. tuberculosis antibodies in a non-human and for raising anti-M. tuberculosis antibodies in a non-human are also used as vaccines MRB12A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding more accounts of the invention are useful as in vivo diagnostic agents.

Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 5.55e-54 675.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

US-09-684-215B-4 (1-132) x AAD28343 (1-2190)

IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 Arcaccecerceacececrocearcaacreesceaceceareecearecescerraac 321 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 20 81 40 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 22 ACGGCCGCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlyGlyGlyThrValHis ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 101 21 82 41 61 202 81 262 121 a ò g ò Db  $\stackrel{>}{\circ}$ g ò g Š 셤 ò

AAL40773 standard; DNA; 2191 RESULT 18 AAL40773

BP.

AAL40773;

entry) (first 03-OCT-2002 Nucleotide sequence encoding Ral2-H9-32A fusion protein.

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.

Unidentified

Chimeric

Key

/*tag= a /product= "Ra12-H9-32A fusion protein" Location/Qualifiers 1. .2190

WO200125401-A2

12-APR-2001

06-OCT-2000; 2000WO-US027652.

07-OCT-1999; 99US-0158585P.

CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. P-PSDB; AAO22142. Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure; Fig 6; 39pp; English.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14 (Mycobacterium theoreulosis, and a heterologous polymucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual is infected with it. The fusion polypeptides are useful as the individual is infected with it. The fusion polypeptides to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polymucleotide sequence in protein. 

Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;

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	5.56e-54	675.00	100.00%	100.00%	100.00%	4
Alignment Scores:	Pred No.:	Score	Percent Similarity:	Best Local Similarity:	Onerv Match:	

US-09-684-215B-4 (1-132) x AAL40773 (1-2191)

417

382 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGGCC

us-09-684-215b-4.rng

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Alignment Scores:
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/transl except= (pos:597. .605, aa:Ala-Gln)
/transl_except= (pos:98. .802, aa:Ala)
/transl_except= (pos:98. aa:Ala)
/transl_except= (pos:98. aa:Ala)
/note= "This codon has an apparent 2 nucleotide insertion
which alters the reading frame"
                                                                                                                                                                   GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                              GlyGlnalaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                           GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG
        IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                           Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
tuberculostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
Ra12-TbH9-Ra35.
                                                                                                                                                                                                                                                                                                              DNA encoding antigenic fusion protein Ral2-TbH9-Ra35 (Mtb32-Mtb39)
                                                                                                                                                                                                    ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                              ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 417
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/product= "Mtb32-Mtb39"
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
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                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Chimeric.
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(first entry)
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A
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18-FEB-1998;
07-APR-1998;
30-DEC-1998;
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08-MAY-2002
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protectin coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis tuberculosis. This sequence represents DNA encoding an M. tuberculosis (use fusion protein of the invention. (Updated on 29-AUG-2003 to standardise os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGGAAGTCTCCGCCATCTCCACCGGCGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 Arcedectracecerreteerreserrisesrereteachacaacaaceaceacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                   useful
                                                                                                                 New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2286 BP; 373 A; 719 C; 807 G; 381 T; 0 U; 6 Other;
Campos-Neto
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Matches:
Conservative:
Mismatches:
Indels:
Alderson M,
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Dillon DC,
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Skeiky YA,
                                          WPI; 2002-171134/22.
P-PSDB; AAU74588.
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Best Local Similarity:
Query Match:
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IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
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27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA sequence includes a coding region for a recombinant Wycobacterium tuberculosis tri-antigen fusion protein (see AA132059), termed Mtb32A, composed of the antigens Ral2, TbH9 and Ra35. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. 3 Coding sequences for Ral2, TbH9 and Ra25 were ligated to encode Mtb32A. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGerProThrValHis 40
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                                                                                                                                                                                                                                                                                                                                                                                                   fusion proteins useful for diagnosis, prevention and treatment of
             Tuberculosis, antigen, fusion protein, Mtb32A, Ra12, TbH9, Ra35, diagnosis, therapy, vaccine, immunogen, ss.
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                                                                                      Location/Qualifiers
42. .2231
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                                                                                                                                                                                                                 99WO-US007717.
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98US-00223040
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675.00
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                                                            Mycobacterium tuberculosis.
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P-PSDB; AAY32059.
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30-DEC-1998;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leif, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion propeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human and man and for raising antibodies in a non-human and man and for raising antibodies in a non-human and man and for raising antibodies in a non-human and man Rais protein from Mycobacterium tuberculosis and TDHS protein from Mycobacterium tuberculosis and TDHS protein from Mycobacterium sp. (Updated on 29-MUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polymuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                         422
                                      GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Vaccine, immunity, diagnostic agent, gene therapy, TbH9; antigen, Ra35;
Ra12; WTB72F; chimeric, gene, ds.
                                                             363 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAACTCGGGGGGCACGGT
                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium sp. MTB72F fusion protein encoding DNA
                                                                                                                                                     458
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                                                                                                                  ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                           423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
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/*tag= a
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Mycobacterium tuberculosis.
Chimeric.
                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
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63 ACGGCCGCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCGATC 122
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              20-JUN-2001; 2001WO-US019959.
                                         20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                  Skeiky Y, Reed S, Alderson
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P-PSDB; AAE17572.
                                                                                   (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                303 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGGATGGCGGGACGCGCTTAAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 GGCCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 422
                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                  302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                                          63 ACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGATTCGCCATTCCGATC 122
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                                                                                                                                                                                                                                                GlyGlnAlaWetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                                                                                                                                                                                                                                              41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                     ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                               243 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAACGTG
                                                                                                                                                                                       ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72F; Ra12-TbH9-Ra35; ds.
              814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium species MTB72F fusion protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
42. .2231
42. .2231
/*tag=
/product= "MTB72F fusion protein"
/*tag= b
/note= "Ra12 DNA fragment"
/*tag= c
/note= "TbH9FL DNA fragment"
/*tag= d
/*tag= d
/*tag= d
/note= "Ra35 DNA fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458
                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                           (1-2287)
              Sequence 2287 BP; 372 A; 717 C;
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                                                                                                                                                            US-09-684-215B-4 (1-132) x AAD47083
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                                                     5.83e-54
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Best Local Similarity:
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                                          Alignment Scores:
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22287 132 0 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

242

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302 100 362 120

101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg

303 ATCACCGCGCTCGACCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC

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WO200198460-A2

27-DEC-2001

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymoulectices are useful as diagnosic tools in partients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as vaccines MyrmalsA insion proteins of the invention are also used as vaccines. Myrcobacterium species MTB72R (Ral2-TDM9-Ra35) fusion protein
                                                                                                                                                                                                                                                                                  Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosiatic; gene therapy; vaccine.
                                                                                                                                      GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                        GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                145 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                          61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGCTTAAC
ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium MTB72F-MTI (fusion MTB83F) protein encoding DNA
                                                                                                                                                                                                                                                                         ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                      385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 2487
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P-PSDB; ADA26366.
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               422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antiqens, with or without the MTB65A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                              ds, gene; fusion protein; MTB32A, MTB39; antigen; MTB32A, MTB39, MTB85A, tuberculosis, tuberculostatic; gene therapy; vaccine.
  " MTB72F-DPV (fusion MTB81F) protein"
                                                                                                                                                                                        Mycobacterium MTB72F-DPV (fusion MTB81F) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2451 BP; 389 A; 785 C; 870 G; 407 T; 0 U; 0 Other;
                                        ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                        423 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                     Location/Qualifiers
4. .2445
/*tag= a
/product= " MTB72F-DI
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                                                                                                               ADA26360 standard; DNA; 2451
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675.00
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P-PSDB; ADA26367.
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                                                                                                                                                                                                                                                                Mycobacterium sp
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Pred. No.:
Score:
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                                       121
                 363
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel nucleic acid encoding a fusion polypopetide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A
                                                                           /*tag= a
product= "MTB72F-MTI (fusion MTB83F) protein"
Location/Qualifiers
4. ,2481
/*tag= a
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ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGhealaIleProIle

(1-2451)

US-09-684-215B-4 (1-132) x ADA26360

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Percent Similarity: Best Local Similarity: Query Match: DB:

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GICCAACGCGIGGICGGGGGGCGCCCCGGCGCAAGICTCGGCATCTCCACCGGCGACGTG 264
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polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                 ThralaalaaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIle
                                                                                                                                                                                                                              25 ACGGCCCCCCCCCCCATAACTTCCCAGCTGTCCCAGGGTGGGCAGGATTCGCCATTCCCATC
                                                                                                                                                                                                                                                                                                                                                                 ValGinArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal
                                                                                                                                                                                                                                                                  GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium MTB72F-Erd14 (fusion MTB89F) protein encoding DNA
                                                              U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "MTB72F-Erd14 (fusion MTB89F)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                             Sequence 2487 BP; 394 A; 784 C; 896 G; 413 T; 0
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4. .2631
/*tag= a
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                                                                                                                             Percent Similarity:
Best Local Similarity:
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DB:
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81 ileThrAlaValAspGlyAlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                                                                 The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A and mTB85A and mTB85A and mTB85A and mTB85A and mTB85A and more of the ruberculosis ocmplex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vecine. The methods and compositions of the present invention as useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                    New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAepVal
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                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                               Sequence 2637 BP; 428 A; 840 C; 928 G; 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-215B-4 (1-132) x ADA2635B (1-2637)
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                                      Reed
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675.00
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(first entry)
                                      Guderian J,
                                                               WPI; 2003-697554/66.
P-PSDB; ADA26365.
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
          CORIXA
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27-JAN-2003
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                                      Skeiky Y,
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DB:
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diagnostic agent; gene therapy; MTB72F; MAPS;

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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA
                                                                                                                                    13-MAR-2002; 2002WO-US008223
                                                                                                                                                  13-MAR-2001; 2001US-0275837P
                                                                                                                                                                               Brannon M,
                                                                                                                                                                                           WPI; 2002-759844/82.
P-PSDB; AAE29731.
                                                                                                                                                                 (CORI-) CORIXA CORP
               Vaccine; immunity;
chimeric; gene; ds.
                                   Mycobacterium sp.
Leishmania sp.
                                                                                                         WO200272792-A2
                                                                                                                       19-SEP-2002
                                                                                                                                                                               Skeiky Y,
                                                  Chimeric
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Guderian J;

/*tag= a /product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95£) fusion protein"

cocation/Qualifiers

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, M15, and 6H polymucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. MTB72F-Leishmania sequence comprises Mycobacterium sp. MTB72F (at 22 kDa poly-protein fusion construct comprising Ral2-TDH9-Ral35) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other; Example 6; Page 128-129; 155pp; English standardise OS field)

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2808
132
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
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      7.36e-54
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US-09-684-215B-4 (1-132) x AAD47110 (1-2808)

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- GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A and MTB95 antigen, or MTB32A, MTB32B and wTB95A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymeclotide of the invention may have a use in gene therapy, and as a practine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                   81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                        264
                                                                                                                                                                             ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
                                                                                                                                                                                                                                              384
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds, gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                      egecarcarcecegricacercarcredereaccredeaaaccaaercegecececer
                                                                                         ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                 101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                       145 Arcaeaccraccaccriccrcactragarantarcacaacaacaacaacaacaacaacacaca
                                  IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium MTB72F-MAPS (fusion r95F) protein encoding DNA.
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product= "MTB72F-MAPS (fusion r95F)"
                                                                                                                                                                                                                                                                                               385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                             ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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P-PSDB; ADA26364.
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Guderian
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Best Local Similarity:
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Skeiky Y,
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                                                                                                                     25 ACGGCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCGATTC
                                                                                                                                                                                                            ValGlnargValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                                          GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
                                                                                                                                                           41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                           ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
         Other;
                                  2808
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/note= "No stop codon given"
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                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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/product= "MTB-120F F
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          BP; 466
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                          Alignment Scores:
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB12A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymerclotide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrhrg
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tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72R; 85B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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Indels:
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US-09-684-215B-4 (1-132) x ADA26362 (1-3104)
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P-PSDB; ADA26369.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antiqens, with or without the MTB35A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                        (fusion MTB103F)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3060 BP; 503 A; 977 C; 1070 G; 510 T; 0 U; 0 Other;
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4. .3054
/*tag= a
                                                                                                                                                                                          "MTB72F
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                                                                  Mycobacterium bovis.
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Query Match:
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB39 antigen, or MTB12A, MTB32A and MTB39 antigen, or MTB12A, MTB32A and MTB39 antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vectine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "MTB72F-hTCC#1 (fusion MTB102tm2F) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3104 BP; 510 A; 968 C; 1104 G; 522 T; 0 U; 0 Other;
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Matches:
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Indels:
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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                      101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrUysSerGlyGlyThrArg 120
                                                                                                                                                                                                                                                      205 GTCCAACGCGTGGTCGCGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAACGTG 264
                                                                                                                                                                                                          265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACGGCGATGGCGGACGCGCTTAAC 324
                                                   85 GGCCAGGCGATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGGTCACCCACGTTCAT 144
                                                                                                                                ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
                            21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
25 ACGGCCGCCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 84
                                                                                                                                                                                                                                                                                                             385 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
                                                                                                                                                                                                                                                                                            121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Search completed: April 29, 2004, 23:03:02 Job time : 382.474 secs

Scoring table:

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Minimum DB Maximum DB

Searched:

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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Mark
APPLICANT: Campos-Neto, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Busion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
                                                                                          Sequence 5, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 18, Applisequence 64, Applisequence 11, Applisequence 12, Applisequence 12, Applisequence 12, Applisequence 182, Applisequen
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Sequence 353, App
Sequence 353, App
5 US-09-287-849-27
5 US-10-359-460-27
6 US-10-098-732A-3
5 US-10-098-732A-5
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Patent No. US20020009459A1
GENERAL INFORMATION:
             447
1872
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      -09-287-849-27
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-TRANS=human40.cdi -LIST=45 - DGCALIGN=200 - THR SCORE=pct - THR MAX=100
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-THR MIN=0 - ALIGN=30 - MODE=LGCAL - OUTFWT=0 - THR PASS CTRE=500 - MINLEN=0
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-NCRU-6 - ICPU=3 - NO MMAP - LARGEQUERY - NEG $\overline{G}$ \overline{G}$ \overline{G}$
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 TAASDNFQLSQGGGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
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1. \cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2. \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3. \cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4. \cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
5. \cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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7. \cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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13. \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
14. \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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16. \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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18. \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19. \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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19. \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                           - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2936184 seqs, 2261732022 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext C
Ygapop 10.0 , Ygapext C
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Query Match Length DB

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; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PRATURE:
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; OTHER INFORMATION: frame 1
; NAME/KEY: CDS
; OCHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
; OTHER INFORMATION: Eading frame 1
; NAME/KEY: CDS
; OCHER INFORMATION: Eading frame 2
; OCHER INFORMATION: Feading frame 2
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; OTHER INFORMATION: reading frame 3
; LOCATION: (2)...(701)
; OTHER INFORMATION: reading frame 3
; LOCATION: (2)...(701)
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Mismatches:
Indels:
Gaps:
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US-10-359-460-27
Sequence 27, Application US/10359460
Sequence 27, Application US/10359460
Publication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
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TITLE OF INVENTION: Pusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE REFERENCE: 0.14058-009020US
CURRENT PLING DATE: 0.14058-009020US
CURRENT APPLICATION NUMBER: US/0/359,460
PRIOR PLING DATE: 1999-04-07/9/289,499
PRIOR PLING DATE: 1999-04-07/9/289,899
PRIOR PLING DATE: 1999-04-07/9/289,899
PRIOR PLING DATE: 1999-04-07/9/289,899
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-12-30
PRIOR PLING DAT
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Indels:
Gaps:
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Sequence 5, Application US/10098732A;
Sequence 5, Application WS/10098732A;
Publication No. US2030175294A1
GENERAL INFORMATION:
APPLICANT: Steiky, Mark
APPLICANT: Glorian, Jeffrey
APPLICANT: Glorian, Jeffrey
APPLICANT: Glorian, Jeffrey
APPLICANT: Glorian, Jeffrey
APPLICANT: Glorian Scoporation
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
FRIOR PLILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
LEMBOTH: 1002
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                                                                                                                                                       Sequence 3, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Glderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologue Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologue Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologue Fusion Protein Constructs
CURRENT APPLICANT: 2010-04-29

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 60/275,837

PRIOR APPLICATION NUMBER: US 60/275,837

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 1002
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                 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCACGCGT 384
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-098-732A-3
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Sequence 15, Application US/09712363
GENERAL INFORMATION:
APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
US-10-098-732A-5
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Mismatches:
Indels:
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101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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Sequence 17, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Leishmania Antigen
FILE REPERENCE: 014058-01201005
FILE REPERENCE: 014058-01201005
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
                                                        APPLICANT: ACCIA, OCTIVA
APPLICANT: CORIX, OCTIVA
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERNOE: 014058-00901US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: mutated
OTHER INFORMATION: MTB32-WTB39F fusion protein (MTB32MutSA)
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US-10-098-732A-17
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: 105(09/712,363)

CURRENT APPLICATION NUMBER: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR PILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/17,844

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-03-6

PRIOR FILING DATE: 1999-03-6

PRIOR PRIOR DATE: 1999-03-6

PRIOR PRIOR DATE: 1999-03-6

PRIOR PRIOR DATE: 1999-03-6

PRIOR PRIOR DATE: 1999-03-6

PRIOR FILING DATE: 1999-03-14

PRIOR FILING DATE: 1999-05-14

PRIOR FILING DATE: 1999-11-12

PRIOR PRIOR DATE: 1999-11-12

PRIOR PRIOR DATE: 1999-11-12

PRIOR PRIOR DATE: 1999-11-12

PRIOR PRIOR DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 292

NUMBER OF SEQ ID NOS: 292

IGNORANISM: Mycobacterium tuberculosis

US-09-712-363-15
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Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
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675.00
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Sequence 1, Application US/09287849

SEQUENCE 1 Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Oblion, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Corixa Corporation

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009020US

FURENT APPLICATION NUMBER: US 08/918,112

PRIOR APPLICATION NUMBER: US 08/918,112

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1997-03-13

PRIOR FILING DATE: 1998-02-10-01

PRIOR PILING DATE: 1998-02-10-01

PRIOR FILING DATE: 1998-02-10-01

PRIOR PILING DATE: 1998-02-10-01

PRIOR FILING DATE: US 08/925,197

PRIOR FILING DATE: US 08/056,556
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                 TYPE: DNA.
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
US-10-098-732A-17
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 2190
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: 130)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 1, Application US/10359460
; Publication No. US20030147911A1
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
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PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 0
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
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                                                                                                              LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: modified_base
LOCATION: (2270)
CTHER INFORMATION: n = 9,
US-09-287-849-1
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Best Local Similarity:
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61 ValGlnArgValValGlySerhlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
303 ATCACCGGGTCGACGGCGCTCCGATCAACTCGGCCACGCGGTTGGCGGGCTTAAC 362
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US-10-088-732A-15
US-10-088-732A-15
Sequence 15, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Goderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION NUMBER: US 0010098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 15
LENGTH: 2287
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                                                                                                        363 GGGCATCATCCCGGTGACGTCACCTCGGTGAACCAACCCAAGTCGGCGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39 OTHER INFORMATION: fusion)
                                                                                                                                                          121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Mismatches:
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NAME/KEY: CDS
LOCATION: (42)...(2231)
OTHER INFORMATION: MTB72F
FEATURE:
NAME/KEY: modified base
LOCATION: (1)...(2287)
OTHER INFORMATION: n = g, a, c or t US-10-098-732A-15
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ORGANISM: Artificial Sequence
FEATURE:
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Query Match:
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Pred. No.:
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  APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Busion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE OF INVENTION: and Their Uses
FILE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR PAPLICATION NUMBER: US 08/918,112
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1998-04-18
PRIOR PELING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR PELING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR PELING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATCHILL US: 2.1
LENGTH: 2287
TYPE: DNA
TYPE: DNA
CREATER: ALTIFICIAL SEQUENCE
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)
FATURE:
NAME/FEE: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
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US-10-359-460-1
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NAME/KEY: CDS
LOCATION: (42)..(2231)
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NAME/KEY: modified base
LOCATION: (33)
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Best Local Similarity:
Query Match:
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DB 183 ATGGGCCTACCGCTTGGGTTTGTCGACAACAACGGCAACGGCCACGA 242  Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80  243 GTCCAACGCGTGGGCTCTGGCGAACTTCCCACGCGACGCACGGCACGGCACGCAC	RESULT 12 US-10-369-983-8 ; Sequence 8, Application US/10369983 ; Publication No. US2003023593A1 ; GRNERAL INFORMATION: ; APPLICANT: Skeiky, Yasir ; APPLICANT: Guderian, Jeff ; APPLICANT: Reed, Steven ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis ; TILE REFERENCE: 014058-00981US ; CURRENT FILING DATE: 2003-02-18 ; FRICR APPLICATION NUMBER: US/10/369,983 ; CURRENT FILING DATE: 2003-02-18 ; RICR APPLICATION NUMBER: US 60/357,351 ; NUMBER OF SEQ ID NOS: 22 ; SOFTWARE: PatentIn Ver. 2.1	ificial Sequence TION: Description of Artif TION: MTB81F (MTB72F-DPV) 3.71e-70 Leng 675.00 Cong 7: 100.00% Macc rity: 100.00% Mine	US-09-684-215B-4 (1-132) x US-10-369-983-8 (1-2451)
29 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 29 303 ATCACCGCGCTCGCATCGCATCGCACCGCACGCGGCGCGCGC	APPLICANT: Algerson, Mark APPLICANT: Algerson, Mark APPLICANT: Corixa Corporation APPLICANT: Corixa Corporation APPLICANT: Corixa Corporation TITILE OF INVENTION: Fuelon Proteins of Mycobacterium tuberculosis Antigens TITILE OF INVENTION: Ruelon Proteins of Mycobacterium tuberculosis Antigens TITILE OF INVENTION: And Their Uses FILE REFERENCE: 014058-00901005 CURRENT FILING DATE: 2003-02-03 CURRENT FILING DATE: 1998-112-30 PRIOR APPLICATION NUMBER: US/09/223,040 PRIOR APPLICATION NUMBER: US/09/223,040 PRIOR APPLICATION NUMBER: US/09/223,040 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO LENGTH: 2287 TYPE: DNA ORGANISM: Artificial Sequence FRATURE: PATURE: OTHER INFORMATION: Description of Artificial Sequence: FRATURE:	OTHER INFORMATION: protein Ral2-TbH9-Ra35 FEATURE: NAME/KEY: modified_base LOCATION: (30) OTHER INFORMATION: n = g, a, c or t FEATURE: NAME/KEY: modified_base LOCATION: (33) OTHER INFORMATION: n = g, a, c or t FEATURE: FEATURE: FEATURE: NAME/KEY: CDS LOCATION: (42)(2231) FEATURE: FEATURE: COTHER INFORMATION: n = g, a, c or t FEATURE: FEATURE	Alignment Scores:  Alignment Scores:  Alignment Scores:  Score:  Conservative:  Best Local Similarity:  100.00%  Mismatches:  Conservative:  100.00%  Mismatches:  100.00%  Mismatches:  100.00%  Mismatches:  100.00%  Mismatches:  100.00%  Indels:  0  Agap:  0  1 ThralahaserAspAsnPheGlnLeuSerGlnGlyGlvGhalalleProile 20

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RESULT 15
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                               101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
                                                  325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTCGGCAAACCAAGTCGGGCGCGCACGCGT 384
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265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 324
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                                                                                                                                                                                 Sequence 7, Application US/10369983
; Sequence 7, Application US/10369983
; Publication No. US20030235893A1
; GENERAL INFORMATION:
   APPLICANT: Skeiky, Yasir
   APPLICANT: Reed, Steven
   APPLICANT: Corixa Corporation
   TITE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
   TILE REFERENCE: 014058-009081US
   CURRENT APPLICATION NUMBER: US $6/357,351
   PRIOR APPLICATION NUMBER: US $6/357,351
   PRIOR FILING DATE: 2002-02-15
   NUMBER OF SEQ ID NOS: 22
   SOFTWARE: Patentin Ver. 2.1
   STO ID NO? 2.2

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RESULT 14
US-10-369-983-6
| Sequence 6, Application US/10369983
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| APPLICANT: Skeiky, Yasir
| APPLICANT: Guderian, Jeff
| APPLICANT: Guderian, Jeff
| APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: UNMBER: US/10/369,983
| CURRENT APPLICATION NUMBER: US/0/357,351
| PRIOR FILING DATE: 2002-02-15
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 6
| LENGTH: 2637
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Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Alignment Scores:
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                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence:WTB72F-WAPS
OTHER INFORMATION: (195f) fusion construct, TB WTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: (1,05f) fusion construct, TB WTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: (178A or MAPS)
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 2003-04-29
CURRENT FILING DATE: 2003-04-29
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEC ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 2808
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Publication No. US20030235593A1
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICANTION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/357,351
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US-10-369-983-5
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Sequence 3, Application US/10369983;
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014089-009081US
CURRENT FILIAG DATE: 2003-02-18
CURRENT FILIAG DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SEQ ID NOS: 22
SEQ ID NO S: 22
                                                                                                                                                                                                                                                                                                                                                               Description of Artificial Sequence:fusion protein R95F (MTB72F-MAPS)
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 2808
TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Bescription of the companion of the compan
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101 GlyHisFisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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FRATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB102tm2F (MTB102FTM, MTB72F-hTCC#1)
US-10-369-983-10
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                        US-09-684-215B-4 (1-132) x US-10-369-983-11 (1-3060)
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ORGANISM: Artificial Sequence
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Sequence 11, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-0098310S

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER: PATENT FILING UNCS: 22

SOFTWARE: PATENT VET. 2.1

SEQ ID NO: 1.

LENGTH: 3060
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: protein US-10-369-983-3
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                                                          81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
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EIP: 99104-7092

COMPUTER: READLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: DATE:

COMPUTER: DATE:

APPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

CLASSIFICATION: (Unknown>

PRIOR APPLICATION: (Unknown>

PRIOR APPLICATION: WOWBER: US/09/072,596

ATTORNEY/AGENT INFORMATION:

NAME: MAK: DAY: 0.5

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET WUMBER: 21,392

REFERENCE/DOCKET WUMBER: 210121.417C9

TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444
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Mismatches:
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Publication No. US20030135026A1
GENERAL INFORMATION:
Section Steiry, Yasir A.W.
Dillon, Davin C.
Campoe-Neto, Antonia Houghton, Raymond Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, Romald C.
Hendrickson, ROMD MET
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TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-193-002-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Washington
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 21
US-10-193-002-4
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                                                                                                                                                                                                                                                                                                                                         265 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGTTAAC 324
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     GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGGTCACCCGTTCAT 144
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                                                                                          IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
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Publication No. US20030235593A1

Publication No. US20030235593A1

SERENATION:

APPLICANT: Skeiky, Vasir

APPLICANT: Guderian, Jeff

APPLICANT: Graderian, Jeff

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014658-009081US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 9

IENGTH: 3474
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Pred. No.:
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US-10-369-983-9
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US-09-684-215B-4 (1-132) x US-10-084-843-4 (1-447)
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
FEFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                           US-09-684-215B-4 (1-132) x US-10-193-002-4 (1-447)
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| Sequence 9, Application US/10098732A
| Publication No. US20030175294A1
| Publication No. US20030175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Xasir
| APPLICANT: Brannon, Mark
| APPLICANT: Guderian, Jeffrey
| APPLICANT: Corize Corporation
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs
| TITLE OF INVENTION: Heterologous Fusion Protein Protein Comparison Protein Prot
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OTHER INFORMATION: Description of Artificial Sequence:WIBRal2 (WTB32A
OTHER INFORMATION: C-terminus)
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA
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Dillon, Davin C.

Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                  447
131
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                                                  Length:
Matches:
Conservative:
Mismatches:
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RPPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

CLASSIFICATION: «UDKNOWN»
                                                                                                                          Indels:
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                       1.86e-70
670.00
99.24%
99.24%
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                    Percent Similarity:
Best Local Similarity:
                                 Alignment Scores:
Pred. No.:
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US-10-193-002-17
US-10-098-732A-9
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998 ATCACCGCGCTCGACGCCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1057
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Skelky, Yasir A.W.
Dillon, Davin C.
Campos Natunio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acadedaacereacarreecceaececceccecces
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NAME: MAXI, DAVIG J.

NAME: MAXI, DAVIG J.

REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LANGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                    670.00
99.24%
99.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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998 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGGACGCGTTAAC 1057
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                                                                                                                  Sequence 1, Application US/10088732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jefffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Grixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
FILE REFERENCE: 014058-01201008;
CURRENT FILING DATE: 2003-04-29
FRIOR FILING DATE: 2003-04-29
FRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1872
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FRATURE:
OTHER INFORMATION: MTB32A (Ra35FL)
FRATURE:
NAME/KEY: modified base
LOCATION: (1) . (1872)
OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                         CITY: Seattle
COUNTR: USA
COUNTR: USA
COUNTR: USA
COUNTR: USA
COUNTR: USA
COMPUTE: READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
COMPUT
                                                                                                                                          Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGGAACGIGACATIGGCCGAGGGACCCCCGGCC 1153
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEE and BERRY LLP
STREET: 6300 Columbia Center,
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LENGTH: 1872 base pairs
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STRANDEDNESS: single
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RESULT 27
US-09-759-143-822
; Sequence 822, Application US/09759143
; Patent No. US20020022248A1
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; TYPE: DNA
; ORGANISM: Homo
US-09-780-669-822
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1126
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APPLICANT: Xu, Jangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Kanos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darick
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darick
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS
CURRENT APPLICATION UNMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SEQ ID NO 8EQ ID NOS: 934
LEMETER HARDER PROBLEMENT NOTES TO NO NOSE TO NOSE TO
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US-09-780-669-822
Sequence 822, Application US/09780669
Patent No. US20020051977A1
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US-09-759-143-822
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APPLICANT: MCABLIL, Patricia D.
APPLICANT: HOUGHLON, RAYMOND L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTHARE: FASTESEQ FOR WINDOWS Version 3.0
SEQ ID NO 822
LENGTH: 675
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                                                              Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
Ku, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer
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Hepler, William
Hural, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
           Sequence 822, Application US/09822827
Sequence 822, Application US/09822827
Gartent No. US2002081680A1
Gartent No. US2002081680A1
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARER: PastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Matches:
Conservative:
Mismatches:
Indels:
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o. US20020192763A1
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                  9.88e-66
632.00
96.21%
95.45%
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; ORGANISM: Homo sapiens
US-09-822-827-822
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Best Local Similarity:
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US-09-895-793-822
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foughton, Raymond L.
AP
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Matches:
Conservative:
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Job time : 493.039 secs
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; ORGANISM: Homo sapiens
US-09-895-793-822
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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

117, Appl 822, App 822, App 1862, App 353, App 834, App 834, App 834, App 831, App 351, App 361, App 3

Sequence Seq

Sequence Sequence Sequence

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Minimum DB Maximum DB

Searched:

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APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corres Corporation Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: A COPPLICANT USES
TITLE OF INVENTION: DATE: 1999-04-07
TITLE OF INVENTION: DATE: 1999-04-07
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR PLICATION NUMBER: US 09/025,556
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 27
THENGTH: 702
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US-09-056-556-17

US-09-072-596-17

US-09-072-596-17

US-09-636-215-822

US-09-636-215-822

US-09-643-597-1862

US-09-643-597-353

US-09-643-597-353

US-09-643-597-353

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US-09-643-597-351

US-09-6443-597-351

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US-09-6443-597-351

US-09-620-412C-348

US-09-620-412C-348

US-09-598-419-382

US-09-598-419-382

US-09-598-419-388

US-09-598-419-388

US-09-598-419-388

US-09-598-419-388

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US-09-50-412C-308

US-09-50-412C-316

US-09-50-412C-316

US-09-50-412C-318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/09287849; Patent No. 6627198; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
        -09-287-849-27
        Sequence 27, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appli
                                                                                                                                                                                 April 29, 2004, 22:28:57; Search time 67.5789 Seconds (without alignments) 1083.969 Million cell updates/sec
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675
1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
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11: / Ggn2 & (ptodate/2/ina/5A_COMB.seq:*
12: / Cgn2 = (ptodate/2/ina/5B_COMB.seq:*
3: / Cgn2 = (ptodate/2/ina/6A_COMB.seq:*
4: / Cgn2 = (ptodate/2/ina/6B_COMB.seq:*
4: / Cgn2 = (ptodate/2/ina/PCTUS_COMB.seq:*
5: / Cgn2 = (ptodate/2/ina/PCTUS_COMB.seq:*
6: / Cgn2 = (ptodate/2/ina/Pate/Ins/Bed:*)
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                  - nucleic search, using frame_plus_p2n model
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US-09-287-640-1
US-09-287-849-1
US-09-103-840A-1
US-09-103-840A-1
US-08-113-4
US-08-818-111-4
US-09-075-556-4
US-09-072-596-4
US-09-072-596-4
US-08-818-111-17
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Listing first 45 summaries
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonio
APPLICANT: Carpos Neto, Antonio
APPLICANT: Ocivis Neto, Antonio
APPLICANTON Fusion Procises of Mycol
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00902003
CURRENT PRILING DATE: 1999-04-07
PRIOR PILING DATE: 1997-03-13
PRIOR PLLING DATE: 1997-03-13
PRIOR PLLING DATE: 1997-03-13
PRIOR FILING DATE: 1998-02-18
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NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c
NAME/KEY: CDS
LOCATION: (42)...(2231)
NAME/KEY: modified_base
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                   COCATION: (1)...(693)
COTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: (2)...(700)
COTHER INFORMATION: reading frame 2
NAME/KEY: CDS
COTHER INFORMATION: reading frame 3
LOCATION: (3)...(701)
COTHER INFORMATION: reading frame 3
US-09-287-849-27
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PRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35
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                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42): (2231)
NAME/KEY: modified_base
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 1
LENGTH: 2287
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                                                                                                                                                                                                                                                                                                                                                            ) IOCATION: (2270)
) OTHER INFORMATION: n = g, a, c
US-09-287-849-1
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675.00
100.00%
100.00%
                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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: modified_base
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Best Local Similarity:
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US-09-103-840A-2
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Sequence 1, Application US/09103840A

Patent No. 6294328

GENERAL INDEMARION:
APPLICANT: FIEISCHAM, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHYER, John C.
TITLE OF INVENTION: TUBRECTOLOSIS
TITLE OF INVENTION: TUBRECTOLOSIS
TITLE OF INVENTION: UNMASER: US/09/103,840A

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                     TYPE: DNA

TYPE: DNA

FRAUME:
FRATURE:
OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152344 AcAdddaAcdrdaCArrddcCdaAdddaCcccCdGCC 152379
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Pred. No.:
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TUBERCULOSIS
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Matches:
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PILLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKL, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411
TELECOMMUNICATION INFORMATION:
TELEPRANC (206) 682-4900
TELEPRAN (206) 682-6031
INFORELEPRAN (206) 682-6031
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INFORELEPRAN (206) 682-6031
INFORELEPRAN (206) 682-6031
INFORENCE CHARACTERISTICS:
LENGTH: 47 Dase pairs
TYPE: mucleic acid
STRANDEDNESS: single
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APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Seeiky, Yasir A.W.

APPLICANT: Canpos-Net, Antonio

APPLICANT: Canpos-Net, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Houghton, Raymond

APPLICANT: Wardick, Thomas S.

APPLICANT: Wardick, Daniel R.

ITILE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

ITILE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IMW FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
                                                                                                                                                                                                                                                                  US-09-684-215B-4 (1-132) x US-09-103-840A-1 (1-4411529)
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                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                              Gaps:
                       ; TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                    2.04e-60
675.00
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                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNBER: 210121.457
REPERRUCE/DOCKET NUMBER: 220121.457
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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US-09-056-556-4
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US-09-072-596-4
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                                                                   COMPUTER FRAAABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: MICHOL'S SINGLE
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Conservative:
Mismatches:
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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Pred. No.:
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US-09-056-556-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE WIMMER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue STREET: Washington
COUNTRY: USA Length: Matches: Conservative: Mismatches: Indels:

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311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCGCACGCGT 370
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251 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Thomas S.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTITILE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
TITLE OF INVENTION:
APPLICANT: USA
ZIP: Washington
COMPUTER: ESD and BERRY LLP
SOFTWARE: PROPENTION:
MEDICATION TYPE: Floppy disk
COMPUTER: PROPENTION: PC-DOS/MS-DOS
SOFTWARE: PREFICATION NUMBER: US/09/072,967
FILING DATE: 05-WAY-1998
CLASSIFICATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/COMPUNICATION NUMBER: 31,392
REFERENCE/COMPUNICATION: 41,000
REMAIN TOTOM NUMBER: 31,392
REFERENCE/COMPUNICATION: 41,000
REMAIN TOTOM NUMBER: 31,392
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos. Meto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Romald C.
APPLICANT: Hendrickenn Romald C.
APPLICANT: Radangton
COUNTRY: Washington
COUNTRY: USA
COMPUTER: RADALE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: BRACANT: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION NUMBER: 31,392
APPLICATION NUMBER: 31,392
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/ATTORNEY/A
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         4, Application US/09072596
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131 ATCGGGCCTACCGCCTTCCTCGGCTTGGGGACAACAACAACAACGGCAACGGCAACGG
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                                                                      41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
                                                                                                                                                                      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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| Patent No. 629069
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Wardzik, Thomias S. |
| TILE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESS: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: A Batentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR.1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAX, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION NUMBER: 210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 ACAGGGAACGIGACATTGGCCGAGGGACCCCGGCC 406
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
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Matches:
Conservative:
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.66e-64
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STRANDEDNESS: single
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ZIP: 98104-7092
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Percent Similarity:
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TOPOLOGY:
US-08-818-112-17
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Pred. No.:
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campoe-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardix, Thomas S.
APPLICANT: Twardix, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bum PC compatible
COMPUTER: Plan PC compatible
COMPUTER: Dar PC compatible
COMPUTER: Dar PC compatible
COMPRANE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLEASIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEFOND: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                           US-09-684-215B-4 (1-132) x US-08-818-112-17 (1-1872)
   Mismatches:
Indels:
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; Sequence 17, Application US/08818111
; Patent No. 6338852
Best Local Similarity: 99.24%
Query Match: 99.26%
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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                              Query Match:
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TUBERCULOSIS
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Sequence 17, Application US/09072596

Patent No. 645836

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Thomas S.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Hendrickson, Ranald C.

APPLICANT: Hendrickson, Ronald C.
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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   210121.457
REFERENCE/DOCKET NUMBER: 210:
TELECHONE: (206) 622-4900
TELEPHONE: (206) 682-631
TELEPAX: (206) 682-631
INFORMATION FOR ENQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TYPE: TOPOLOGY: linear
                                                                                                                                                                                                                               2.66e-64
670.00
99.24%
99.24%
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STATE: Washington
                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                     Alignment Scores:
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DB:
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                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                  2.66e-64
670.00
99.24%
99.24%
   LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDENBESS: single
COPCLOGY: linear
US-08-818-111-17
                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                   Alignment Scores:
Pred. No.:
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US-09-056-556-17
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

CLASSIFICATION NUMBER: 13,392

ATTORNEY/AGENT INFORMATION:

NAME: MAK!, David J.

REGISTRATION NUMBER: 210121.417C9

TELEPHATION NUMBER: 210121.417C9

TELEPHATION INFORMATION:

TELEPHAX: (206) 692-6931

INFORMATION FOR EQUID NO: 17:

SEQUENCE CHRACTERISTICS:

LENGTH: 1872 base pairs

TOPOLOGY: linear
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Matches:
Conservative:
Mismatches:
Indels:
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Nero, Antonio
Houghton, Raymond
Vedvick, Thomas S.
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Sequence 17, Application US/09072967
Patent No. 652887
GENERAL INFORMATION:
GENERAL Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
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              APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS NO TUBERCULOSIS
NUMBER OF SEQUENCE: 355
CORRESPONDENCE ADDRESS:
ADDRESSED: SEED and BERRY LLP
                                                                                                                                                                 STREET: 6300 COlumbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTY: Washington COUNTY: USA COUNTY: USA COMPTER READABLE FORM: WEDLIN TYPE: Floppy disk COMPUTER: IEM PC COMPATION CONFUTER: DATE: PACENTIN PC-DOS/NS-DOS SOFTWARE: PACENTIN RC-BEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: CURSIT APPLICATION UNMER: US/09/072,967 FILING DATE: 05-MAY-1998
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                                                                                                                                              3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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NAME: MAKI, David J.
REGISCHATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-691
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
Twardzik, Daniel R.
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42722.
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 822
LENTH: 675
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; Sequence 822, Application US/09685166A
; Patent No. 6630305
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, William
TILLGNI: Sheiky, William
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42177017
CURRENT APPLICANON NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SETUND NO 822
LENGTH: 675
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                                                                                                                                                                                                                Sequence 822, Application US/09636215
Patent No. 6620922
                                                                                                                                                                                                                                                                                                                                                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jenninger L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Ratter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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; ORGANISM: Homo sapiens
US-09-636-215-822
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US-09-636-215-822
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US-09-606-421B-353
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370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
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                                                                                         Sequence 1862, Application US/09736457

Patent No. 6509448

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary
APPLICANT: Panger, Gary
APPLICANT: Nedes, Michael A.
APPLICANT: Nedes, Marc
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Wang, Ajun
APPLICANT:
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US-09-643-597-353
Sequence 353, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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CRGANISM: Homo sapiens
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                                                                                              APPLICANT: Funger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Weag, Aljun
APPLICANT: Realsy, Yasir A.W.
APPLICANT: McNeill, Patrica D.
APPLICANT: McNeill, Patrica D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C11
FILE REPERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
SOFTWARE: FREUERQ for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
LENGTH: 900
LENGTH: 900
LENGTH: DNA
COGANISM: Homo sapiens
US-09-643-597-353
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Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Panger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 2012.142717C17
CURRENT PELING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-834
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Patent No. 663030N:
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert P.
PLICANT: Henderson, Robert A.
PLICANT: Raios, Michael D.
'ILCANT: Raios,
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  APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeaky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hallocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Reter, Michael D.
APPLICANT: Reter, Michael D.
APPLICANT: Reter, Michael D.
APPLICANT: Robert A.
APPLICANT: Robert A.
APPLICANT: Conf. M.
APPLICANT: Conf. John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Cater, Darrick
APPLICANT: Li, Samuel
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632.00
96.21%
95.45%
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Best Local Similarity:
Query Match:
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US-09-636-215-834
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Pred. No.:
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APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LINGWOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478615
CURRENT APPLICATION NUMBER: US/09/736,457
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEC ID NOS: 898
SOFTWARE: FastSEC for Windows Version 3.0
SEC ID NO 834
LENGTH: 915
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Patent No. 6509448
GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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CORGANISM: Homo sapiens
US-09-685-166A-834
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101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Rangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: MANGERIA A.W.
APPLICANT: MANGERIA A.W.
APPLICANT: MANGERIA A.W.
APPLICANT: MANGERIA A.W.
APPLICANT: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND MANGER: ASCALL
CURRENT FILING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 351
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WANGER OF SEA
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Matches:
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Mismatches:
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GURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1861
LENGTH: 945
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                                                                                                                                                                                                                                                          1,61e-60
632.00
96.21%
95.45%
                                                                                                                                  TYPE: DNA
CRGANISM: Homo sapiens
US-09-736-457-1861
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Best Local Similarity:
Query Match:
DB:
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Mon May 3 U6:35:U9 Zu

; ORGANISM: Homo sapiens US-09-643-597-351

93.63%

Query Match: DB:

> 81 IleThrAlaValAspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120 235 GTCCAACGCGTGGTCGGCGAGCGCTCCGGCGCAACTCTCGGCATCTCCACCGGCGACGTG 294 295 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGATCAAC 354 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 US-99-00-421B-351
> Sequence 351, Application US/09606421B
> Sequence 351, Application US/09606421B
> Setent No. 6531315
> GENERAL INFORMATION:
> APPLICANT: Wang, Tongtong
> APPLICANT: Fan, Liquin
> APPLICANT: Fan, Chicael D.
> APPLICANT: Fanger, Cart R.
> APPLICANT: Mang, Allun
> SAPLICANT: Mang, Allun
> FILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
> TITLE OF INVENTION: COMPOSITIONS AND INSTRUMENT APPLICATION NUMBER: US/09/606,421B
> CURRENT FILING DATE: 2000-06-28
> NUMBER OF SEQ ID NOS: 359
> SOFTWARE: FastSEQ for Windows Version 3.0
> SEQ ID NO 351
> LENGTH: 1012 121 ThrGlyAsnValThrLeuAlaGluGlyBroProAla 132 415 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 450 Length: Matches: Conservative: Mismatches: Indels: US-09-684-215B-4 (1-132) x US-09-643-597-351 (1-1012) 632.00 96.218 93.458 TYPE: DNA CORGANISM: Homo sapiens US-09-606-421B-351 Percent Similarity: Best Local Similarity: Query Match: DB: RESULT 25 US-09-606-421B-351 Alignment Scores: Pred. No.: Alignment Scores: Pred. No.: g 임 Dp à 유 ò a ò ò ઠે g à g  $\delta$

Length: Matches: Conservative: Mismatches:

1.76e-60 632.00 96.21% 95.45%

Score: Percent Similarity: Best Local Similarity:

US-09-684-215B-4 (1-132) x US-09-620-412C-348	Oy 1 ThraladlaGerAspAsn
; NUMBER OF SEQ ID NOS: 898 . SORTWINDER PRACTICE OF Windows Version 3.0	JOSTANO 851 LENGTH: 1203 TYPE: DNA ORGANISM: HOME SADIENS

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yserProThrValHis 40
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                          SerProThrValHis 40
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370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405

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101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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Fatent No. 656586
GENERAL INFORMATION:
APPLICANT: SCHOLler, John
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: LAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: UNMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: PRESENCE: 357
SOFTWARE: PRESENCE OF Windows Version 3.0/4.0
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Best Local Similarity:
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US-09-598-419-348
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LENGTH: 1464
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           US-09-620-412C-332

Sequence 332, Application US/09620412C

Sequence 332, Application US/09620412C

Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C7

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE FastSEQ for Windows Version 3.0/4.0

LENGTH: 1557
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BD274032 Sequences
AX00578B Sequence
BD274033 Sequence
BD2731322 Pused pro
AR303127 Sequence
AR403735 Sequence
AR403735 Sequence
AR40373 Sequence
BX248334 Mycobacte
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AR233037 Sequence
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-MODEL=frame+ p2n.mcdel -DEV=xlh
-Q=CGGT2 1/VSPTO epocl/USO684215/runat 29042004_061304_13185/app_query.fasta_1.1180
-Q=CGGT2 1/VSPTO epocl/USO684215/runat_29042004_061304_13185/app_query.fasta_1.1180
-Q=CGGT2 1/VSPTO epocl/USO684215/runat_29042004_061304_13185/app_query.fasta_1.1180
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR ECORE=pcr - THR MINED - ALIGN=30 -MODE=LOCAL
-OUTFWT=ptc -NORM=&Xt -HEAPSIZE=50 -MINEDN=0 -MXLEN=200000000
-USER=USO9684215_@CGN_11_6034_@cnunat_29042004_061304_13185 -NCPU=6 -ICPU=3
-NO MAXP -LARGEQUERY -NEG SCORES=0 - WAIT -DSPELOCK=100 -LONGLOG
-DBV TINEDUT=120 -THRANY TIMEDUT=30 -THRANDS=1 -XGAPPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
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1511.672 Million cell updates/sec
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651
1 TAASDNFQLSQGGGFAIPI......SVTWQTKSGGTRTGNVTLAE 128
                                                                                                                                                           April 29, 2004, 20:32:52; Search time 3670.05 Seconds
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                               - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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BD274032 1068 bp DNA linear PAT 17-JUL-2003 Sequences nuclieic acid from polypeptides exportes from mycobacteries, vector the comprehant and applications at diagnostic and the prevention from the tuberculose.
                                                                                                                                                                                                                  PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
(Loases 1 to 702)
Red, S.G., Skeiky Y.A., Dillon, D.C., Alderson, M. and Campos-Neto, A. Fusion proteins of Mycobacterium tuberculosis antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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Location/Qualifiers
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/mol_type="genomic DNA"
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JP 2002510494-A/13.
synthetic construct
synthetic construct
artificial sequences.
[Loases 1 to 702]
Skeiky,Y.A.W., Alderson,M. and Neto,A.C.
Fused protein of Mycobacterium tuberculosis antigen and utilization
thereof
                                                                                                                                                                                                                                                                                                                                     OCTIVE CONTRACTOR

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mtb24), reading frame 1
bi-fusion protein Ra12-DPPD (designated Mtb24),reading frame 1
reading frame 2
reading frame 3
                  BD251334 17-JUL-2003 These protein of Mycobacterium tuberculosis antigen and utilization thereof.
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/organism="synthetic construct"
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PN JP 2002534956-A/256
PN JP 2002534956-A/256
PN 22-CCT-2002
PF 14-AUG-1999 JP 2000509849
PF 14-AUG-1997 FR 97/10404,11-SEP-1997 FR 97/11325 PI
BRIGHTER GICOUEL, DEBNIS PORTHOL, BNG-MONG LIM, VLADIMIR PELICIC, PI
AGNES GIGGUET DE LA SALMONIERE
PC C12N15/09, A61K39/04, A61K48/00, A61P11/00, A61P31/04, CO7K14/35, PC C07K16/12,
PC C07K16/12,
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PC C07K19/00,C12N1/21,C12P21/02,C12Q1/68,G01N33/50, PC G01N33/53/,
PC G12N15/09,C12R1:32),C12N15/00,(G12N15/00,C12R1:32) CC 50D
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                                          Mycobacterium tuberculosis
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Corymebacterinese; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
I (bases I to 1068)
Gioquel, B., Portnoi, D., Lim, E., Pelicic, V., Guigueno, A. and
Salmoniere, Y.G. D.L.
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/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref≈"taxon:1773"
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/note="unnamed protein product; 50D"
/codon start=1
/transl_table=11
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/db_xref="REMTREMBL.CACOS178"
/db_xref="REMTREMBL"
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Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for disgnosing and preventing tuberculosis Patent: WO 9909186-A 907 25-FEB-1999;
PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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Matches:
Conservative:
Mismatches:
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Sequence 907 from Patent WO9909186.
AX005788 1 GI:9928795
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Polygoptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 9909186-A 909 25-FBB-1999;
PORTNOI DENIS (FR); GUICUENO AGNES (FR)
Location/Qualifiers
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VGGGGATAPAQAAPPALSOBRADPFALEDPBANAQAQBOVYNINTAGYNNAVGA
GGGGATAPAQAAPPALSOBRADPFALEDPBANAQAQBOVYNINTAGAYNAVGA
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PINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAAGGPPA.
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925 GTCCAACGCGTGGGTGGGGGCTCCGGCGGCAAGTCTCCGGCATCTCCACCGGCGACGTG 984
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterinae, Mycobacteriaceae, Mycobacterium, Mycobacterium
tuberculosis complex.
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/note="unnamed protein product; SEQ ID NO 50F"
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/organism="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
/db_xref="taxon:1773"
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/protein_id="CAC05179.1"
/b_xref="G1;9928798"
/db_xref="REMTREMBL:CAC05179"
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/transl_table=:
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/mol_type="genomic DNA"
/db_xref="taxon:1773"
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                                                                                                                                  123 GGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT 182
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Skeiky,Y., Alderson,M. and Campos-Neto,A.
Fusion proteins of mycobacterium tuberculosis antigens and their
     1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
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Location/Qualifiers
1.2287
/organism="unknown"
/mol_type="genomic DNA"
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Sequence 1 from patent US 6544522.
AR303127
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PN JP 2002510494-A/1

PD 09-APR-1999 US 09/056556,30-DEC-1998 US 09/223040 PI

PR 07-APR-1999 US 09/056556,30-DEC-1998 US 09/223040 PI

YASIR A W SKEIXY,MARK ALDERSON,ANTONIO CAMPOS NETO PC

C12P21/02,

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Mycobacterium tuberculosis CDC1551

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymbacterinaes, Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

I (bases 1 to 14029)
S Fleischmann, K.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salaberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
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E (Dassel 1 to 14029)

F leischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Gwinn, M., Haft, D., Hickey, E., Foolary, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Kolonay, J.F., Nelcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Wikula, A. and Bishai, W.

Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

Location/Qualifiers

1. 14029

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gene="MT0131"
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AE006925 AE000516
AE006925.1 GI:13879610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [ (bases 1 to 2287)
Reed, S.G., Skeiky, Y.A., Dillon, D.C., Alderson, M. and Campos-Neto, A. Fusion proteins of Mycobacterium tuberculosis antigens and their
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243 GICCAACGCGIGGICGGAGGCGCICCGGCGAAGICTCGGCAICICCCACCGGCGACGIG 302
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Location/Qualifiers
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Sequence 1 from patent US 6627198.
AR403735.1 GI:40151411
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VERNRAAFCDGYAVASGIDPRDSALLLGAYELDKAVYETGGSTRHRFGWLPIPLRSIR
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id="AAK44359.1"
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/gene="MT0138"
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/producTe=8erine protease, putative"
/producTe=8erine protease, putative"
/producTe=8erine protease, putative"
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NNGNGARAVQRVGAPAASLGISTGDVITAVDGAPINSATAMADAINGHHPGDVISUT
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4695. .6500
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6695. .6500
/ gene="MT0.14"
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/ fene="mT0
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ASSELRLAREREAMIL PGGKGLSGGSAHSPAVQVVVSKATHAKLKELARSRKMSVSKL
LRPVLDEFVQRETGRILPRR"
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/gene="MT0132"

/note="similar to GB:AL123456; identified by sequence

/software identified by sequence

/codon start=1

/transl_table=11
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/gene="MT0133"
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/gene="MT0135"
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/transl_table=11 /product="pep2_protein"

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Gramus J.C., Pryor M.J., Medigue C., Cole S.T.;
"Re-annocation of the genome sequence of Mycobacterium tuberculosis H37Rv";
Microbiology 148:2967-2973(2002).
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ALO21930; AL123456; Z74410; Z80233; Z80775; Z86089; Z92669; Z92770; Z96071;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry III C.E., Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G."Deciphering the biology of Mycobacterium tuberculosis from the complete
      81 ileThralaValaspGlyalaProlleAsnSeralaThralaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                                                                          GlyHisHisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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                                                                                                                                                                                                                                                4428 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCCACCGCGATGGCGGACGCGCTTAAC
                                                                        IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                             ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.
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(Rel. 77, Last updated, Version 1)
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MEDLINE; 98295987.
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Submitted (24-MRX-2003) Garnier T., Unite de Genetique Moleculaire
Bacterienne Institut Pasteur 28,rue du Dr Roux 75724 PARIS cedex
15, France. e-mail:tgarnier@pasteur.fr Submitted on behalf of the
Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
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Mycobacterium bovis subsp. bovis AF2122/97
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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PNAS 10.1073/pnas.1130426100 (Microbiology)
2 (bases 1 to 343050)
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KEYWORDS
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//note="Rv0003, (MTCY10H4.01), len: 385 aa. recF, DNA
replication and repair protein (see citations below),
equivalent to orders Mycobacterial DNA replication and
repair proteins e.g. NP 301131.1|NC 0026/7 from
mycobacterium apture (385 aa); Q9L7D5|RECF MYCPA from
Mycobacterium apture (385 aa); D5096|RECF MYCSM from Mycobacterium aregments (385 aa);
P5096|RECF MYCSM from Mycobacterium aregments (385 aa);
p5096|RECF MYCSM from Mycobacterium snegments (384 aa);
etc. Also highly similar to others e.g. p36176|RECF STRCO
DNA REPLICATION AND REPAIR PROTEIN from Streptomyces
coelicolor (373 aa); NP 446982.1|NC 000991 from
Synechocystis sp. strain PCC 6803 (384 aa);
NP 469352.1|NC 003212 from Listeria innocua (370 aa); etc.
Contains PS00017 ATP(GTP-binding site motif A (P-loop),
PS00617 RecF protein signature 1, and PS00618 RecF protein
signature 2, BELONGS TO THE RECF FAMILY."
                                                                                                         /EC_numDer="12,7,7,"
/function="DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN
BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5'
EXONUCLEASE ACTIVITY. THE BETA CHAIN IS REQUIRED FOR
INITIANION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA, IT
BUIDES FREELY (BIDIRECTIONAL AND ATP-INDEPENDENT) ALONG
LYPDROSPHATE = N diphosphate + {DNA}N]."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /procein_id="CAA16219.1"
/translation="MDAATTRVGLTDLTFRLLRESFADAVSWVARNLPARPAVPVLSGV
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NRVALTGGNAFRSLPTMPVBDYPTLPTFRTELRBAFTBLAM
LTGTRVBTLGSTVGVATDAATDRFRLAVRELKWSASSPDIEBANVPPAKTLARAAKGGTGG
DVRLSLGTGPGVGKDGLLGISGNGKRSTTRLLDAEFPKFRQLLPTEHTAVATMDVAELI
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TRDYVGYLRAYLFAPEDLGLYRGDPADRRRYLDDLAIYRRPAIAAVRAEYERYLRGRTA
LLKSYPGARYRGDRGYFDTLEYWDSRLAEHGAELYAARIDLYNQLAPEVKKAYQLLAPE
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($INGLE-STRAND DNA BINDING PROTEIN)"
protein -"MYD024241"
franslation="MYD2HIGLRDPRSWACUDLELHPGRTVFVGPNGYGKTNLIEALWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRSASI GYRASMDVTGPSEQSDI DRQLLAARLLAALAARRDAELERGVCLVGPHRODLI
LRLGDQPAKGFASHGEAWSLAVALRLAAYQLLRVDGGEPVLLLDDVFAELDVMRRRALA
TAAESAEQVLVTAAVLEDI PAGWDARRVHI DVRADDTGSMSVVLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAIKLVALVADRGAQVRMEFADGSVRLSAGADDVGRAEEDLVVDYAGEPLTIAFNPTYL
TDGLSSLRSERVSFGFTTAGKPALLRPVSGDDRPVAGLNGNGPPPAVSTDYVYLLMPVR
   in 337 aa overlap); P21174|DP3B_MICLU from Micrococcus Luctus (310 aa); P52023|DP3B_SYMP7 from Synechococcus sp. strain PCC 7942 (375 aa); etc. Overlaps and extends CDS in neighbouring cosmid MICY10H4.01."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM AND RECOMBLINATION, IT IS REQUIEDED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECF BINDS PERFERBNITALLY TO SINGIR-STRANDED, LINEAR DNA. IT ALSO SEEMS TO BIND AFP."
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/evidence=EXPERIMENTAL
/evidence=EXPERIMENTAL
/norde="Rv0004, (MTCY10H4.02), len: 187 aa. Conserved
/norde=itcal procein (see Salazar et al., 1996), highly
similar, but longer 21 aa in N-terminus, to
AAF33696.1|AF222789 unknown protein from Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLITRANSFERASE)"
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/note≈"PS00017 ATP/GTP-binding site motif A"
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'note≈"PS00617 RecF protein signature l"
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/note≈"PS00618 RecF protein signature 2"
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151936

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9

FEATURES

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/Jocus taga "MADONOI"
//Jocus "MADONOI daa, from Mycobacterium tuberculosis strain H37Rv, (99.6% identity in 507 aa overlap). ChaA, chromosomal replication intiator protein (see citations below), equivalent to other Mycobacterial CHROMOSOMAL REPLICATION INITIATOR PROTEINS e.g. P46388 |DNAA MYCLE from Mycobacterium paratuberculosis (502 aa); P49992 |DNAA MYCRA from Mycobacterium paratuberculosis (503 aa); P49992 |DNAA MYCRA from Mycobacterium snegmatis (504 aa); Q91771 |DNAA MYCRA from Mycobacterium snegmatis (504 aa); P49992 |DNAA MYCRA from CHROMOSOMAL REPLICATION INITIATOR PROTEIN from Streptomyces carrysomallus (624 aa); Q92H75 |DNAA STRRH to others except in N-terminus e.g. Q92H75 |DNAA STRRH from Streptomyces carrysomallus (624 aa); Q92H76 |DNAA STRRE from Streptomyces catrysomallus (624 aa); Q92H76 |DNAA STRRE from Streptomyces catrysomallus (624 aa); Q92H76 |DNAA STRRE from Streptomyces reticuli (643 aa); DNAA ECOLI |P03004 |B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa); ABARA SCOLI |P03004 |B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa); ABARA SCOLI |P03004 |B3702 chromosomal replication initiator protein sequence interfactoria supmature. BELONGS TO THE DNAA FAMILY. Note that the first base of this gene has been taken as base 1 of the Mycobacterium bovis genomic sequence."
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/Jocus tag="Mb0002"
/Jocus tag="Mb0002, dnaN, len: 402 aa. Equivalent to Rv0002, dnobe="Mb00002, dnaN, len: 402 aa. Equivalent to Rv0002, len: 402 aa, from Mycobacterium tuberculosis strain H37Rv, (99.8% identity in 402 aa overlap). dnaN, DNA polymerase III (beta chain) (EC 2.7.7.7) (see citations below), equivalent to other Mycobacterial DNA POLYMERASES II BETA CHAIN e.g. NP 301130 I NC 002677 from Mycobacterium leprae (399 aa); Q9LTL6 | DP3B MYCPA from Mycobacterium avium subsp. paratuberculosis (399 aa); PS2851 | DP3B MYCSM from Mycobacterium avium conters e.g. P27903 | DP3B RRCD NA POLYMERASE III BETA COAPERS e.g. P27903 | DP3B MYCPA from Subspromyces coelicolor (376 aa); PRATA scores: Opt: 1189, E(): 0, (52.8% identity in 337 aa overlap);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trainlation="MTDDPGSGFTTVWNAVVSELNGDPKVDDGPSSDANLSAPLTPQORAMINUVQPLTIVEGFALLSYPSSTVQNEIERHLRAPITDALSRELGHQIQUGVRIAP
PATDEADDTTVUPSERNATTSPDTTTNDEIDDSAARGONGNSWPSYFTERRRNTDS
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BGKEGIQEBFFHTFWTHNANKQIVISSDRPPKQATLREBERRFRFRFRFRFTFDK
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CRELIDLSLANGARRALADANGARRALAGSRQIAMYL
Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone, Jaurey KTIS 3NB, UK. Sanger Centre, Wellcome Trusts Genome Campus, Hinxton, Cambridge CBio 18A, UK. PT4 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France. Location/Qualifiers
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(protein_id="CAD92863.1"
(db_xref="GI:31616763"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Mycobacterium bovis subsp. bovis AF2122/97"
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'transl_table=11
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2052. 3260
/gene="dnaN"
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. .1524
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/gene≂"dnaN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="dnaA"
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gene

CDS

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CDS

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SOURCE
ORGANISM
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/Jocus_tag="wb0005"
/Eorniber="5.99.1.3"
/For number="5.99.1.3"
/For nu
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Matches:
Conservative:
Mismatches:
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Sequence 4 from patent US 6290969.
AR169152 48169152.1 GI:17906927
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651.00
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Best Local Similarity:
Query Match:
DB:
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AR169152
LOCUS
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ACCESSION
VERSION
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PAT 20-APR-2002
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(bases 1 to 447).

Vedo, S. Skeiky, Y.A.W., Dillon, D.C., Ca Vedvick, T.S. and Twardzik, D.R.

Compounds and methods for diagnosis of to S338822-A 4 15-JJN-2002;
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I (bases 1 to 447)
Reed,S.G., Skekky,Y.A.W. and Dillon,D.C.
Compositions and methods for the prevention and treatment of M.
tuberculosis infection
Patent: US 6330456-4 4 26-PEB-2002;
Location/Qualifiers
                                                                                         ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyBlaAlalleProlle
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Vedylck, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for diagnosis of tuberculosis

Patent: US 6458366-A 4 01-0CT-2002;

Location/Qualifiers
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PAT 21-JUN-2002

RESULT 17
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ORGANISM REFERENCE AUTHORS

JOURNAL FEATURES

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Reed,S.G., Skeiky,Y.A., Dillon,D.C., Campos-Neto,A., Houghton,R.L., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis Perculosis P 1203817-A 4 08-MAY-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 4 from Patent EP1203817.
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for immunotherapy and diagnosis of tuberculosis patent: US 6592877-A 4 15-UUL-2003;
Location/Qualifiers

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4 from patent US 6592877.
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for diagnosis of Tuberculosis
Contract: JP 2001500383-A 4 16-JAN-2001;
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 Compounds for immunotherapy and diagnosis of tuberculosis Patent: EP 1347055-A 4 24-SEP-2003; CORIXA CORPATION (US) Location/Qualifiers
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BD006325.1 GT:18634696
UP 2001S00383-A/4.
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Compounds and methods for immunotherapy and diagnosis of Tuberculosis.

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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.

Compounds and methods for immunocherapy and diagnosis of Patent: JP 2001501832-A 4 13-FEB-2001;

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FN JP 2001501832-A/4

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PC C12N15/31, C07K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62,
PC C07K19/00,
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                     RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI
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PP 02-077-2001

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PP 08-523436,22-SEP-1995 US 08/533634 PR 08/521996 US 08/620974,05-JUN-1996 US 08/659683 PR 12-JUL-1996 US 08/680574

PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
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PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC CIZNIS/10,

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PC CIZNI/21, AGIRS/10, (CIZNI/21, CIZRI:19)

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Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-OCT-2001; CORIXA CORP
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SM Unknown.
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SE Red(S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis tuberculosis.
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311 GGGCATCATCCCGGTGACGTCATCTCGGTGAACTGGCAAACCAAGTCGGGCGGCGCGCGT 370
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                                              ThrGlyAsnValThrLeuAlaGlu 128
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PC 68,
PC G01N13/569,G01N13/68//A61K38/00,A61K39/04,A61K39/395,A61K39/PC 395,A61P31/06,
PC (C12N1/21,C12R1:19),C12N15/00,C12N5/00,A61K37/02 CC Compounds and methods for diagnosis of tuberculosis. FH Key Location/Qualifiers
                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium
tuberculosis complex.
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PN 17-2EP-2002
PD 17-EEP-2002
PF 17-FEB-1999 JP 2000532132
PR 18-FEB-1998 US 09/024753,05-MAY-1998 US 09/072596 PI
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI
NETO,
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                                                                                                                                             1 (bases 1 to 447)
Reed, S.G., Skeiky.Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R. Vedvick,T.S., Twardzik,D.R., Lodes,M.J. and Hendrickson,R.C. Compounds and methods for diagnosis of tuberculosis
Patent: 1P 2002530050-A 4 17-SEP-2002;
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1. 447
/ organism="Mycobacterium tuberculosis"
/ organism="Mycobacterium tuberculosis"
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/ db_xref="taxon:1773"
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JP 2002530050-A/4.
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Mycobacterium tuberculosis
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Unclassified.
1 (bases 1 to 1872)
Reed,S.G., Skeiky,Y.A.W. and Dillon,D.C.
Compositions and methods for the prevention and treatment of M. tuberculosis infection
Patent: US 6350456-A 17 26-FEB-2002;
Location/Qualifiers
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I (bases 1 to 1872)
Reed, S.G., Skelky, Y.A.W., Dillon, D.C., Campos-Neto, A., I Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis Patent: US 6338852-A 17 15-JAN-2002;
Location, Qualifiers
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AR194838.1 GI:20244275
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RS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
Compounds and methods for diagnosis of tuberculosis
Compounds and methods for diagnosis of tuberculosis
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Location/Qualifiers
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Sequence 17 from patent US 6458366.
AR233110.
AR233110.1 GI:27275546
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Compounds and methods for immunotherapy and diagnosis of Puberulosis
Patent: EP 1201817-A 17 08-MAY-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                938 GTCCAACGCGTGGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGGAAGTG
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| Redd, S. G., Skeiky, Y. A. W., Dillon, D. C., Campos-Neto, A., Houghton, R.,
| Redd, S. T. Wardzik, D. R., Lodes, M. J. and Hendrickson, R. C.
| Compounds and methods for immunotherapy and diagnosis of
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